

3-
81

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DESCRIPTION	Homo sapiens epitheliasin (TMPRSS2) mRNA, complete cds.			
ACCESSION	AF329454			
VERSION	AF329454.1	GI:14091027		

[illegible]

15916
TITLE
Cloning and characterization of the cDNA and gene for human epitheliasin
JOURNAL
Eur. J. Biochem. 268 (9), 2687-2699 (2001)
MEDLINE
21223025

REFERENCE	2 (pages 1 to 3420)
AUTHORS	Jacquinet, E., Rao, N.V., Rao, G.V., Wang, Z., Albertine, K.H. and

TITLE Direct Submission
JOURNAL Submitted (15-DEC-2000) Pulmonary Medicine, University of Utah,
50N. Medical Dr., Salt Lake City, UT 84132, USA
FEATURES Location/Qualifiers
2000

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/chromosome="21"
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/gene="TMPRSS2"
128..1606
CDS

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Best Local Similarity	99.68;	Pred. No. 0;		
Matches 3188; Conservative	0;	Mismatches	8;	Indels 6; Gaps 5;

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 15, 2003, 08:38:25 ; Search time 631 Seconds
(without alignments)
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Searched: 2185239 seqs, 112599159 residues
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	3331.8	96.8	3483	ABV27570
6	3331.8	96.8	3483	ABV27589
7	3331.8	96.8	3483	ABV29119
8	3330.2	96.7	3483	ABV24651
9	3330.2	96.7	3483	ABV29165

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12	3136.8	91.1	3245	22	AA564178	Human prostate cDN
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14	3136.8	91.1	3245	24	ABL95549	Human P1000C cDNA
15	2309.4	67.1	2479	21	AAZ90478	Ovrlis homolog pro
16	2309.4	67.1	2479	21	AAZ87813	Human tumour supp
17	2309.4	67.1	2479	22	AA564164	Human cDNA encodin
18	2309.4	67.1	2479	22	AAAD13168	Human serine prote
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20	2309.4	67.1	2479	24	ABK92201	Prostate cancer-as
21	2309.4	67.1	2479	24	ABL95535	Human transmembran
22	2309.4	67.1	2479	24	AAAD28779	Human TMPRSS2 gene
23	1710.4	49.7	1738	21	AAZ29636	Human 20P1F12-GTC2
24	1710.4	49.7	1738	21	AAAD28778	Human 20P1F12-GTC1
25	1468	42.5	1479	21	AAZ87786	Human tumour supp
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45	490	14.2	557	24	ABL95183	Human P1000C cDNA

ALIGNMENTS

RESULT 1
AAZ95005
ID AAZ95005 standard; cDNA; 3443 BP.
AC AAZ95005;
XX
DT 15-AUG-2000 (first entry)
XX
DE Cancer specific gene Prol15 useful as prostate cancer marker.
XX
KW Prostate cancer; cancer specific gene; CSG; diagnosis; monitoring;
KW staging; imaging; therapy; metastasis; marker; human; Prol15; ds.
XX
OS Homo sapiens.
XX
PN WO200023111-A1.
XX
PD 27-APR-2000.
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PF 19-OCT-1999; 99WO-US24331.
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PR 19-OCT-1998; 98US-0104737.
XX
PA (DIAD-) DIADEXUS LLC.
XX
PI Salceda S, Recipon H, Cafferkey R;
XX WPI: 2000-339531/29.
XX
PT Diagnosing, staging and monitoring the presence and metastases of
PT prostate cancer especially useful for treating prostate cancer
PT comprises measuring changes in cancer specific gene levels -

XX Claim 7, page 57-58, 74pp: English.
 XX The present sequence is that of a full-length contig for cancer
 CC specific gene (CSG) Pro15 (clone 2189835H1): a corresponding
 CC expressed sequence tag is given in AA295004. The CSG was identified
 CC in a database search using the data mining Cancer Leads Automatic
 CC Search Package (CLASP), which allows the identification of highly
 CC expressed organ and cancer specific genes. Overexpression of
 CC Pro109 was observed in 3 of 4 primary prostate cancer tissues
 CC examined, indicative of it being a diagnostic marker for prostate
 CC cancer. The invention provides ESTs and full-length contigs for
 CC prostate CSBs (see AA24998-295017). The CSBs, polypeptides encoded
 CC by them, and antibodies that specifically bind CSG are used in new,
 CC claimed methods for detecting, diagnosing, monitoring, staging,
 CC imaging and treating prostate cancer. The new methods provide
 CC earlier diagnosis for the presence and metastasis of prostate
 CC cancer, and can be used to determine if a cancer has metastasized,
 CC or to monitor the progress or stage of the disease when it has not
 CC metastasized.
 CC
 XX
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 1441 AGGGAAGCTGATGATCTTGTGAGAGGAGTGAAGAGGCTCTGCTACTTGAAGAAACA
 1441 AGGGAAGCTGATGATCTTGTGAGAGGAGTGAAGAGGCTCTGCTACTTGAAGAAACA
 1501 AGGGAAGCTGATGATCTTGTGAGAGGAGTGAAGAGGCTCTGCTACTTGAAGAAACA
 1501 AGGGAAGCTGATGATCTTGTGAGAGGAGTGAAGAGGCTCTGCTACTTGAAGAAACA
 1561 ATATCTGTGCTGATGATGAGGAGTGAAGAGGCTCTGCTACTTGAAGAAACA
 1561 ATATCTGTGCTGATGATGAGGAGTGAAGAGGCTCTGCTACTTGAAGAAACA
 1621 CAGAGGTATAGGAGATGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 1621 CAGAGGTATAGGAGATGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 1681 CAGAGGTATAGGAGATGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 1681 CAGAGGTATAGGAGATGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 1741 TTTTGTCTTCCCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 1741 TTTTGTCTTCCCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 1800 TTTTGTCTTCCCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
 1800 TTTTGTCTTCCCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT

QY 1751 ACTTGTCTGGCTTTGGCACTCTCTGCAATCTGTGACAGCTGACGTGCTCCCTGCCCA 1810
 |||||
 Db 1812 ACTTGTCTGGCTTTGGCACTCTCTGCAATCTGTGACAGCTGACGTGCTCCCTGCCCA 1871
 |||||
 QY 1811 GCTGTCTCCCTTAACCCCTTGTCCGCAAGGGGTGATGGCCGGCTGGTGTGGGCACTGG 1870
 |||||
 Db 1872 GCTGTCTCCCTTAACCCCTTGTCCGCAAGGGGTGATGGCCGGCTGGTGTGGGCACTGG 1931
 |||||
 QY 1871 CGGTCAAGTGTGGAGAGAGAGGGGTGGAGGCTCCCATTTAGATCTTCTGCTGATGCT 1930
 |||||
 Db 1932 CGGTCAAGTGTGGAGAGAGAGGGGTGGAGGCTCCCATTTAGATCTTCTGCTGATGCT 1991
 |||||
 QY 1931 TTCCAGAGGGCCAAATTTGGATAGCATGAGCTGTACCTCTCAGCTGTGATGATCTTG 1990
 |||||
 Db 1992 TTCCAGAGGGCCAAATTTGGATAGCATGAGCTGTACCTCTCAGCTGTGATGATCTTG 2051
 |||||
 QY 1991 AATATGAAAAAGAGAGACATGTGAAAAAGGGAGACAGCCAGGTGACCTGACGCGGCTGCC 2049
 |||||
 Db 2052 AATGAAAAAGAGAGACATGTGAAAAAGGGAGACAGCCAGGTGACCTGACGCGGCTGCC 2111
 |||||
 QY 2050 TCTGGGGCCACTTGTGATGTCTCCAGCTTACCTCTCACAAGAGGGATTTTGTGATGG 2109
 |||||
 Db 2112 TCTGGGGCCACTTGTGATGTCTCCAGCTTACCTCTCACAAGAGGGATTTTGTGATGG 2171
 |||||
 QY 2110 TTCTTAGAGCCTTACAGACCCCTGATGTGGCCAGAAATTAAGAGACCAAGCCCTTCATGG 2169
 |||||
 Db 2172 TTCTTAGAGCCTTACAGACCCCTGATGTGGCCAGAAATTAAGAGACCAAGCCCTTCATGG 2231
 |||||
 QY 2170 GTGGTACGTGGTATGACCTTGTAAAGGGGAACAGAAATTTTCTTAAAGGGGTGA 2229
 |||||
 Db 2232 GTGGTACGTGGTATGACCTTGTAAAGGGGAACAGAAATTTTCTTAAAGGGGTGA 2290
 |||||
 QY 2230 GAATATAGACAGTGCCTTGGGTGCGAGGGGAAGCAATTGAAAAAGAACTTGCCTTAGCA 2289
 |||||
 Db 2291 GAATATAGACAGTGCCTTGGGTGCGAGGGGAAGCAATTGAAAAAGAACTTGCCTTAGCA 2349
 |||||
 QY 2290 CTCCTGTGTGACAGTCTCCACCTGTGACATTTGGTGGGGCTCTCTGGAGGAGACTACGCT 2349
 |||||
 Db 2350 CTCCTGTGTGACAGTCTCCACCTGTGACATTTGGTGGGGCTCTCTGGAGGAGACTACGCT 2409
 |||||
 QY 2350 TCTCTCTCATCTCCCTGTGACCTGTCTAGCAACCTGTGAGAGTGCACATGGCCCTTGGT 2409
 |||||
 Db 2410 TCTCTCTCATCTCCCTGTGACCTGTCTAGCAACCTGTGAGAGTGCACATGGCCCTTGGT 2469
 |||||
 QY 2410 CCTGGGCAAGGGGCGCAAGTCTGTGCAACATGTGGCTCTTCAAGGCTGCTAGTACTGG 2469
 |||||
 Db 2470 CCTGG--CAGGGGCGCAAGTCTGTGCAACATGTGGCTCTTCAAGGCTGCTAGTACTGG 2527
 |||||
 QY 2470 AAATTAGAGTCCATGGGGGAATCAAGATGCTCAGTTTAAGGTACACGTGTTCCATGTT 2529
 |||||
 Db 2528 AAATTAGAGTCCATGGGGGAATCAAGATGCTCAGTTTAAGGTACACGTGTTCCATGTT 2587
 |||||
 QY 2530 ATGTTTCTACATGCTGCTACCTGCTCAGTGTCTGGAAGAACTAGCTTTTGAATGCTCCAAGT 2589
 |||||
 Db 2588 ATGTTTCTACATGCTGCTACCTGCTCAGTGTCTGGAAGAACTAGCTTTTGAATGCTCCAAGT 2647
 |||||
 QY 2590 AGTCCACCTTCAATTAATCTTTGAACATGATCATCTTTGCAAGTAAGAGTGTGGCC 2649
 |||||
 Db 2648 AGTCCACCTTCAATTAATCTTTGAACATGATCATCTTTGCAAGTAAGAGTGTGGCC 2707
 |||||
 QY 2650 TATTTACAGTCTTGTGACAAATGACTGCTCCTGACTTAAGCTTATTAATGAATGTG 2709
 |||||
 Db 2708 TATTTACAGTCTTGTGACAAATGACTGCTCCTGACTTAAGCTTATTAATGAATGTG 2767
 |||||
 QY 2710 CTGAAGCAAAAGTCCATGATGTGGGGGGAAGAAAGATGTGTTTGTGTTGAGCTC 2769
 |||||
 Db 2768 CTGAAGCAAAAGTCCATGATGTGGGGGGAAGAAAGATGTGTTTGTGTTGAGCTC 2827
 |||||
 QY 2770 TCTGTGTCTCTTCAATCTGTGGGTTTCAACAGGGGAAGGGTCCCTTTTGCATTTG 2829
 |||||
 Db 2828 TCTGTGTCTCTTCAATCTGTGGGTTTCAACAGGGGAAGGGTCCCTTTTGCATTTG 2887
 |||||
 QY 2830 CAATGTCCATTAACCATGAGCACTACTCTACATGTTTGTGCTCTGTGGCCAAAGCAGCTG 2889
 |||||

Db 2888 CAATGTCCATTAACCATGAGCACTACTACTACATGATGTCTGCTCCCTGCGCAACAGGCTG 2947
 |||||
 QY 2890 GTTTGCAAGAAATGAATGATGATCTTACAGCTAGAGACTTAACCTGAAATGGAAGTCT 2949
 |||||
 Db 2948 GTTTGCAAGAAATGAATGATGATCTTACAGCTAGAGACTTAACCTGAAATGGAAGTCT 3007
 |||||
 QY 2950 TGCATCCCATTTTGCAGAGATCCCTGTGTGACATGCGCTGTGTGAGAGAGCAATTTCCAG 3009
 |||||
 Db 3008 TGCATCCCATTTTGCAGAGATCCCTGTGTGACATGCGCTGTGTGAGAGAGCAATTTCCAG 3067
 |||||
 QY 3010 GGAACCTTGGAAACAGTTGGCAGCTGTAAAGTGTGCTCCCAAGACACATCTTAAAGGT 3069
 |||||
 Db 3068 GGAACCTTGGAAACAGTTGGCAGCTGTAAAGTGTGCTCCCAAGACACATCTTAAAGGT 3127
 |||||
 QY 3070 GTTGTATGTGTGAAACGTTCTCTTATTTATGCCCCCTTCTTATTTATGTGAAACAAGT 3129
 |||||
 Db 3128 GTTGTATGTGTGAAACGTTCTCTTATTTATGCCCCCTTCTTATTTATGTGAAACAAGT 3187
 |||||
 QY 3130 TTTGTCTTTTGTATCTTTTAAACCTGTAAGTTCAATTTGTGAAAAATGATATCATG 3189
 |||||
 Db 3188 TTTGTCTTTTGTATCTTTTAAACCTGTAAGTTCAATTTGTGAAAAATGATATCATG 3247
 |||||
 QY 3190 CAATTAATTAATGCGATTTTTCACAAAGTAACACATGATCTTTGAAGTGTGCTGG 3249
 |||||
 Db 3248 CAATTAATTAATGCGATTTTTCACAAAGTAACACATGATCTTTGAAGTGTGCTGG 3307
 |||||
 QY 3250 TGAATGAGACCAAGCCCAATTTCTTATAAGGGGGGATGTGAGGCTGCTGACAGAG 3309
 |||||
 Db 3308 TGAATGAGACCAAGCCCAATTTCTTATAAGGGGGGATGTGAGGCTGCTGACAGAG 3367
 |||||
 QY 3310 ACCAAGGTGAGGCAAGGCGCAGACTTGTGCTCTGCTGTGTGGTGGCCCTCAGTTCGCA 3369
 |||||
 Db 3368 ACCAAGGTGAGGCAAGGCGCAGACTTGTGCTCTGCTGTGTGGTGGCCCTCAGTTCGCA 3426
 |||||
 QY 3370 GCTGTCTCTGTGAGAGGTCCTCAATGACCTCTTATTTATTTATTTAGTCTG 3426
 |||||
 Db 3427 GCTGTCTCTGTGAGAGGTCCTCAATGACCTCTTATTTATTTATTTAGTCTG 3483
 |||||

RESULT 3
 ABV21767
 ID ABV21767 standard; cDNA; 3483 BP.
 XX
 AC ABV21767;
 XX
 DT 13-SEP-2002 (first entry)
 XX
 DE Human prostate expression marker cDNA 21758.
 XX
 KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
 KW pharmacogenomic marker; gene: ss.
 OS Homo sapiens.
 XX
 PN WO200160860-A2.
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US05171.
 XX
 PR 17-FEB-2000; 2000US-183319P.
 PR 16-MAR-2000; 2000US-189862P.
 PR 25-MAY-2000; 2000US-207454P.
 PR 09-JUN-2000; 2000US-211314P.
 PR 18-JUL-2000; 2000US-219007P.
 PR 13-DEC-2000; 2000US-255281P.
 XX
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX
 PI Schlegel R, Endege WO, Monahan JE;
 XX
 DR WPI; 2001-662795/76.

Db 1812 AATTGCTGCGCTTGGGACATCTCTGCAATTCGTGCAAGGCTGCAAGGCTCCCTGCCCCA 1871
Oy 1811 GCGTCTCTCCCTAACCCCTTGTCCGCAAGGGTGTATGGCCGGCTGGTGGGCACTGG 1870
Db 1872 GCGTCTCTCCCTAACCCCTTGTCCGCAAGGGTGTATGGCCGGCTGGTGGGCACTGG 1931
Oy 1871 CGGTCAAGTGTGGAGAGAGGGGTGGAGGCTCCCAATTTGAGATCTTCTGCTGAGTCT 1930
Db 1932 CGGTCAAGTGTGGAGAGAGGGGTGGAGGCTCCCAATTTGAGATCTTCTGCTGAGTCT 1991
Oy 1931 TTTCAGAGGGGCCAATTTTGTATGAGCATGAGATGTCACCTCTCAGCTGTGATGACTTG 1990
Db 1992 TTTCAGAGGGGCCAATTTTGTATGAGCATGAGATGTCACCTCTCAGCTGTGATGACTTG 2051
Oy 1991 AGATCAAAAAGAGAGACATGTGAAAAGGAGACAGCAGGCTGGACCTGGACGGGGTGC-CC 2049
Db 2052 AGATCAAAAAGAGAGACATGTGAAAAGGAGACAGCAGGCTGGACCTGGACGGGGTGC-CC 2111
Oy 2050 TCTGGGGCCACTTGGTATGTGTCGCCAGCCTACCTCTCCACAAGGGGATTTTGTGATGGG 2109
Db 2112 TCTGGGGCCACTTGGTATGTGTCGCCAGCCTACCTCTCCACAAGGGGATTTTGTGATGGG 2171
Oy 2110 TTCTTAGAGCCTTACAGCAGCCCTGGATGGTGGCCAGAAATTAAGGGACCCCTTCATGG 2169
Db 2172 TTCTTAGAGCCTTACAGCAGCCCTGGATGGTGGCCAGAAATTAAGGGACCCCTTCATGG 2231
Oy 2170 GTGGTAGCTGTAGTACCTCTGTAAAGGGAAACAGAAATTTTGTCTTAATGGGGTGA 2229
Db 2232 GTGGTAGCTGTAGTACCTCTGTAAAGGGAAACAGAAATTTTGTCTTAATGGGGTGA 2290
Oy 2230 GAATATAGACAGTGCCTTGGGTGGCAGAGGAAGCAATTTGAAAAGAACTTGGCCCTGAGCA 2289
Db 2291 GAATATAGACAGTGCCTTGGGTGGCAGAGGAAGCAATTTGAAAAGAACTTGGCCCTGAGCA 2349
Oy 2290 CTCCTGGTGTACAGTCTCCACCTGTGCACATTTGGTGGGGCTTCCTGGGAGGAGACTACGCT 2349
Db 2350 CTCCTGGTGTACAGTCTCCACCTGTGCACATTTGGTGGGGCTTCCTGGGAGGAGACTACGCT 2409
Oy 2350 TCCCTCTCATCTCCCTGTGACCTGTGCTTAGACACCCTGGAGATGACATGCCCCCTTGGT 2409
Db 2410 TCCCTCTCATCTCCCTGTGACCTGTGCTTAGACACCCTGGAGATGACATGCCCCCTTGGT 2469
Oy 2410 CCTGGGAGAGGGGCGCAAGTCTGGCAACCATTTGGCCCTTTCAGGCGCTGTAGTCACTGG 2469
Db 2470 CCTGGGAGAGGGGCGCAAGTCTGGCAACCATTTGGCCCTTTCAGGCGCTGTAGTCACTGG 2527
Oy 2470 AAATTGAGGTCCATGGGGGAAATCAAGATGCTCAGTTTAAAGGTACATGTTTCCATGTT 2529
Db 2538 AAATTGAGGTCCATGGGGGAAATCAAGATGCTCAGTTTAAAGGTACATGTTTCCATGTT 2587
Oy 2530 ATGTTTCTACATTTGCTACCTCAGTGCCTGGAAGAACTTAGCTTTGATGCTCCCAAT 2589
Db 2588 ATGTTTCTACATTTGCTACCTCAGTGCCTGGAAGAACTTAGCTTTGATGCTCCCAAT 2647
Oy 2590 AGTCCACCTTCATTTAACTCTTTGAAGCTGTATCATCTTTGGCCAAGTAAAGAGTGTGGCC 2649
Db 2648 AGTCCACCTTCATTTAACTCTTTGAAGCTGTATCATCTTTGGCCAAGTAAAGAGTGTGGCC 2707
Oy 2650 TATTTACGTGCTTTGACAAATGACTGGCTCTGACTTAACTTATTAATGAATGTTG 2709
Db 2708 TATTTACGTGCTTTGACAAATGACTGGCTCTGACTTAACTTATTAATGAATGTTG 2767
Oy 2710 CTGAAGCAAAAGGCGCATGTGGGCGGCGAAGAAAGAAAGATGTTTGTGTTTGGACATC 2769
Db 2768 CTGAAGCAAAAGGCGCATGTGGGCGGCGAAGAAAGAAAGATGTTTGTGTTTGGACATC 2827
Oy 2770 TCTGTGTGTCCTTCCATGCTGTGGTTCACAACCAAGGGAGGGTCCCTTTGCAATTCG 2829
Db 2828 TCTGTGTGTCCTTCCATGCTGTGGTTCACAACCAAGGGAGGGTCCCTTTGCAATTCG 2887
Oy 2830 CAAGTCCCATTAACCATGAGCACTACTCTACATGTTTGCCTCTGGCCCAAGCAGGCTG 2889

Db 2888 CAAGTCCCATTAACCATGAGCACTACTCTACCATGTTTGCCTCTGCGCCAAAGCAGGCTG 2947
Oy 2890 GTTTGCAAGAAATGAATGAATGATTTCTACAGCTAGGACTTAACCTTGAATGGAAGTCT 2949
Db 2948 GTTTGCAAGAAATGAATGAATGATTTCTACAGCTAGGACTTAACCTTGAATGGAAGTCT 3007
Oy 2950 TGCATATCCATTTTGCAGGATCCGTCTGTGCACATGCGCTGTGAGAGAGCAGCAATTCG 3009
Db 3008 TGCATATCCATTTTGCAGGATCCGTCTGTGCACATGCGCTGTGAGAGAGCAGCAATTCG 3067
Oy 3010 GGCATCTTGAACAGTGTGGCAGCTGTAAAGTGTGCTCCGCAAGACATCTTGAAGT 3069
Db 3068 GGCATCTTGAACAGTGTGGCAGCTGTAAAGTGTGCTCCGCAAGACATCTTGAAGT 3127
Oy 3070 GTTGTATGATGTAAGAAAGCTCTCTCTTATATGCCCCCTCTATTTATGTAAGCAACTG 3129
Db 3128 GTTGTATGATGTAAGAAAGCTCTCTCTTATATGCCCCCTCTTATTTATGTAAGCAACTG 3187
Oy 3130 TTTGTCTTTTGTATGATCTTTTAACTGTAAAGTTCATTTGTGAATGAATATCATG 3189
Db 3188 TTTGTCTTTTGTATGATCTTTTAACTGTAAAGTTCATTTGTGAATGAATATCATG 3247
Oy 3190 CAAATTAATTAATGCAATTTTTCAAAGTAAACCACTGATCTTTGAAGTTCGCTGG 3249
Db 3248 CAAATTAATTAATGCAATTTTTCAAAGTAAACCACTGATCTTTGAAGTTCGCTGG 3307
Oy 3250 TGAATAGAGACAGCTCCATTTCTTATTAAGGGGGGATGTTAGGCTGCTGGTCAAGG 3309
Db 3308 TGAATAGAGACAGCTCCATTTCTTATTAAGGGGGGATGTTAGGCTGCTGGTCAAGG 3367
Oy 3310 ACCAAAGGTGAGGCAAGGCGCAGACTGTGCTGCTGTGTTGGCCCTCAGTTCGCA 3369
Db 3368 ACCAAAGGTGAGGCAAGGCGCAGACTGTGCTGCTGTGTTGGCCCTCAGTTCGCA 3426
Oy 3370 GCGTGTCTGTGTGAGAGGTCCTCAATGATCTCTTATTTATTTATTAAGTCTG 3426
Db 3427 GCGTGTCTGTGTGAGAGGTCCTCAATGATCTCTTATTTATTTATTAAGTCTG 3483

RESULT 4
ABV23318
ID ABV23318 standard; cDNA: 3483 BP.
XX
AC ABV23318;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 23309.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
PD
XX 23-AUG-2001.
XX
PF 20-FEB-2001: 2001WO-US05171.
XX
XX 17-FEB-2000: 2000US-183319P.
PR 16-MAR-2000: 2000US-189862P.
PR 25-MAY-2000: 2000US-207454P.
PR 09-JUN-2000: 2000US-211314P.
PR 18-JUL-2000: 2000US-219007P.
PR 13-DEC-2000: 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JE;
XX
XX WPI: 2001-662795/76.
XX

Db 1812 ACTGTCTGGCTTTGGCACTCTCTGCAATTCGTGCAAGGCTGCAAGTCCCTCCCTCCCA 1871
Qy 1811 GCCGTCTCCCTAACCCCTTGTCCGCAAGGGTGATGGCCGGCTGTTGTGGGCACTGG 1870
Db 1872 GCGTGTCTCCCTAACCCCTTGTCCGCAAGGGTGATGGCCGGCTGTTGTGGGCACTGG 1931
Qy 1871 CCGTCAAGTGTGAGAGAGAGGGGTGAGGCTGCCCATTTGAGATCTTCTGCTGATCCT 1930
Db 1932 CCGTCAAGTGTGAGAGAGAGGGGTGAGGCTGCCCATTTGAGATCTTCTGCTGATCCT 1991
Qy 1931 TTCGAGGGGCAATTTTGGATGAGCATGGAGCTGTCACTCTCAGCTGCTGGATGATCTTG 1990
Db 1992 TTCGAGGGGCAATTTTGGATGAGCATGGAGCTGTCACTCTCAGCTGCTGGATGATCTTG 2051
Qy 1991 AGATGAAAAAGAGAGACATGGAAGAGAGACAGCCAGGTGGCAGCTGAGCGGCTG-CC 2049
Db 2052 AGATGAAAAAGAGAGACATGGAAGAGAGAGACAGCCAGGTGGCAGCTGAGCGGCTGAGCGG 2111
Qy 2050 TCTGGGGCCACTTGGTATGATGTCGCCAGCCTACCTCTCCACAGAGGGATTTTGTGATGGG 2109
Db 2112 TCTGGGGCCACTTGGTATGATGTCGCCAGCCTACCTCTCCACAGAGGGATTTTGTGATGGG 2171
Qy 2110 TTCCTTAGAGCCTTGAAGCCCTGGATGATGGGAGAAATTAAGGGAGCAGCCCTTCATGG 2169
Db 2172 TTCCTTAGAGCCTTGAAGCCCTGGATGATGGGAGAAATTAAGGGAGCAGCCCTTCATGG 2231
Qy 2170 GTGTGAGCTGTGTAGTACCTCTGTAAAGGGAGACAGAACATTTTGTCTTATGGGGTGA 2229
Db 2232 GTGTGAGCTGTGTAGTACCTCTGTAAAGGGAGACAGAACATTTTGTCTTATGGGGTGA 2290
Qy 2230 GAATATAGACAGTGGCCTTGGGTGGGAGGAGAACATTTGAAAAAGAACTTGGCCTGAGCA 2289
Db 2291 GAATATAGACAGTGGCCTTGGGTGGGAGGAGAACATTTGAAAAAGAACTTGGCCTGAGCA 2349
Qy 2290 CTCGAGTGTGAGTGTGCAACCTGACATTTGGGGGGCTCTGGGGAGGAGTCAAGCCG 2349
Db 2350 CTCGAGTGTGAGTGTGCAACCTGACATTTGGGGGGCTCTGGGGAGGAGTCAAGCCG 2409
Qy 2350 TCCTCTCTATCTCCCTGACCTGACCTGTCTTACGACCCCTGGAGAGTGCATGCCCCCTTGGT 2409
Db 2410 TCCTCTCTATCTCCCTGACCTGACCTGTCTTACGACCCCTGGAGAGTGCATGCCCCCTTGGT 2469
Qy 2410 CCTGGGAGAGGGGCGCCAGTGTGGGACCAATGTTGGCCTTTCAGGCGCTGTAAGTCACTGG 2469
Db 2470 CCTGG--CAGGGCGCCCAATGTGTGGCACATGTTGGCCTTTCAGGCGCTGTAAGTCACTGG 2527
Qy 2470 AAATGAGGTCCATGGGGGAAATCAAGATGCTCAAGTAAAGTAAAGTTCATGTT 2529
Db 2528 AAATGAGGTCCATGGGGGAAATCAAGATGCTCAAGTAAAGTAAAGTTCATGTT 2587
Qy 2530 ATGTTCATACATTTGCTACCTGCTAGTGTCTGGAAGAACTTGTGATGATGCTCCAGT 2589
Db 2588 ATGTTCATACATTTGCTACCTGCTAGTGTCTGGAAGAACTTGTGATGATGCTCCAGT 2647
Qy 2590 AGTCAACCTTCAATTTAATCTTTGAAACTGTATCATCTTGGCCAGTAAAGTGTGGCC 2649
Db 2648 AGTCAACCTTCAATTTAATCTTTGAAACTGTATCATCTTGGCCAGTAAAGTGTGGCC 2707
Qy 2650 TATTTACGTGCTTTGACAAATGATGCTGCTCTGACTTAAGCTTATATAAAGATGATG 2709
Db 2708 TATTTACGTGCTTTGACAAATGATGCTGCTCTGACTTAAGCTTATATAAAGATGATG 2767
Qy 2710 CTGAAGCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2769
Db 2768 CTGAAGCAAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2827
Qy 2770 TGTGTGTGCTCTTCCATGCTGTGGTTTCCAAACAGGGGAAAGGCTCTTTTGCATGG 2829
Db 2828 TGTGTGTGCTCTTCCATGCTGTGGTTTCCAAACAGGGGAAAGGCTCTTTTGCATGG 2887
Qy 2830 CAAGTGCCATTAACAGTACACTACTACTACTACTACTACTACTACTACTACTACTACTACT 2889
Db 2888 CAAGTGCCATTAACAGTACACTACTACTACTACTACTACTACTACTACTACTACTACTACT 2947

Qy 2890 GTTTCAGAGATGAATGAATGATGATCTACAGCTAGACATTAACCTTGAAATGGAAGTCT 2949
Db 2948 GTTTCAGAGATGAATGAATGATGATCTACAGCTAGACATTAACCTTGAAATGGAAGTCT 3007
Qy 2950 TGCATATCCATTTTGACAGATCCCTCTGTGTGACATGCTCTGTGTGAGAGACAGCTTCCAG 3009
Db 3008 TGCATATCCATTTTGACAGATCCCTCTGTGTGACATGCTCTGTGTGAGAGACAGCTTCCAG 3067
Qy 3010 GGACCTTGGAAACAGTTGGACATGTAAAGTGTGCTGCTCCCAAGACATCTTAAAGGT 3069
Db 3068 GGACCTTGGAAACAGTTGGACATGTAAAGTGTGCTGCTGCTCCCAAGACATCTTAAAGGT 3127
Qy 3070 GTTGTATGCTGAAACAGTCTTCTCTTATTTATGCCCCCTTCTTATTTATGTAACAAGT 3129
Db 3128 GTTGTATGCTGAAACAGTCTTCTCTTATTTATGCCCCCTTCTTATTTATGTAACAAGT 3187
Qy 3130 TTTGTCTTTTGTATCTTTTAACTGTAAGTCAATTTGTGAATGAAATATCATG 3189
Db 3188 TTTGTCTTTTGTATCTTTTAACTGTAAGTCAATTTGTGAATGAAATATCATG 3247
Qy 3190 CAATTAATATGATGATTTTTCATTAAGTAACTGATCTTGAAGTTCGCTGG 3249
Db 3248 CAATTAATATGATGATTTTTCATTAAGTAACTGATCTTGAAGTTCGCTGG 3307
Qy 3250 TGAATAGACACACCTTCATTTCTTATAAGGGGGTATGATGAGCTGCTGAGAG 3309
Db 3308 TGAATAGACACACCTTCATTTCTTATAAGGGGGTATGATGAGCTGCTGAGAG 3367
Qy 3310 ACCAAAGGTGAGCAAGGCCAGCTTGTGCTCTCTGTGTGTTGCTCCTGATCTGCA 3369
Db 3368 ACCAAAGGTGAGCAAGGCCAGCTTGTGCTCTCTGTGTGTTGCTCCTGATCTGCA 3426
Qy 3370 GCGTGTCTGTGTGAGAGGTCCTCAATGATGCTCTTATTTATTTATTTAGTCTG 3426
Db 3427 GCGTGTCTGTGTGAGAGGTCCTCAATGATGCTCTTATTTATTTATTTAGTCTG 3483

RESULT 5
ABV27570
ID ABV27570 standard; cDNA; 3483 BP.
XX
AC ABV27570;
XX
KW 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 27561.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
XX
OS pharmacogenomic marker; gene; ss.
XX
PN Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001MO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
XX
PR 16-MAR-2000; 2000US-189862P.
XX
PR 09-MAY-2000; 2000US-207454P.
XX
PR 09-JUN-2000; 2000US-211314P.
XX
PR 18-JUL-2000; 2000US-219007P.
XX
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JB;
XX
PI WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of

PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 5634-5635; 11750pp; English.

XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV6211) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 3483 BP: 801 A; 860 C; 938 G; 884 T; 0 other;

Query Match 96.8%; Score 3331.8; DB 23; Length 3483;

Best Local Similarity 99.6%; Pred. NO. 0;

Matches 3403; Conservative 0; Mismatches 7; Indels 7; Gaps 6;

OY 11 GAGCGAGTAGGCGGAGCTAAGCAGAGAGCGGAGGCGGAGGCGGAGGCGGAGG 70
DB 73 GGTGAGTAGAGCGCCAGCTTAAGCAGAGAGCGGAGGCGGAGGCGGAGGCGGAGG 132
OY 71 AGCGCGCGCTGAGCGCGCGAGGCTATTTGAACATTCAGATACCTATCTACTGAT 130
DB 133 AGCGCGCGCTGAGCGCGCGAGGCTATTTGAACATTCAGATACCTATCTACTGAT 192
OY 131 GCTGTGATTAACAGAAATGGCTTTGAACCTCAGGCTCACCACCGCTATTGGACCTTAC 190
DB 193 GCTGTGATTAACAGAAATGGCTTTGAACCTCAGGCTCACCACCGCTATTGGACCTTAC 252
OY 191 TATGAAACCATGATACCAACCGGAAACCCCTATCCGACAGCCGCTGCTGCC 250
DB 253 TATGAAACCATGATACCAACCGGAAACCCCTATCCGACAGCCGCTGCTGCC 312
OY 251 ACTGTCTAGAGAGTGCATCCGGCTCAGTACACCGCTCCCGGCGCCAGTACGCGCG 310
DB 313 ACTGTCTAGAGAGTGCATCCGGCTCAGTACACCGCTCCCGGCGCCAGTACGCGCG 372
OY 311 AGGTCCTGAGGAGGCTTCCAAACCCGCTGCTGTCAGCAGCAGCCCAATCCCATCCGGG 370
DB 373 AGGTCCTGAGGAGGCTTCCAAACCCGCTGCTGTCAGCAGCAGCCCAATCCCATCCGGG 432
OY 371 ACAGTGTGACACTCAAAAGCTAAGAAAGCAGTGTGATACCTTGACCTGGGAGCTTC 430
DB 433 ACAGTGTGACACTCAAAAGCTAAGAAAGCAGTGTGATACCTTGACCTGGGAGCTTC 492
OY 431 CTCTGGAGAGCTGGCGCTGGCGCTGCTACTCTGGAAGTTTCATGAGGAGCAAGTGTCC 490
DB 493 CTCTGGAGAGCTGGCGCTGGCGCTGCTACTCTGGAAGTTTCATGAGGAGCAAGTGTCC 552
OY 491 AACTCTGGAGATAGAGTGGAGCTCTCAGAGTACCTGATCAACCCCTCTAAGCTGTGTAT 550
DB 553 AACTCTGGAGATAGAGTGGAGCTCTCAGAGTACCTGATCAACCCCTCTAAGCTGTGTAT 612
OY 551 GCGGTGACACTGCGCGGCGGAGGAGAGCAAGATGGTGTGCTGCGCTCAGGAGCA 610
DB 613 GCGGTGACACTGCGCGGCGGAGGAGAGCAAGATGGTGTGCTGCGCTCAGGAGCA 672
OY 611 AACTTCATCTTCAAGTGTACTCATCTCAGAGAGAGTCTCTGACACCTGTGTGCCAAGAC 670
DB 673 AACTTCATCTTCAAGTGTACTCATCTCAGAGAGAGTCTCTGACACCTGTGTGCCAAGAC 732
OY 671 GACTGGAACGAGAACTACGGGCGGCGGCTGCAAGGACATGGGCTATTAAGATATTTT 730

DB 733 GACTGGAACGAGAACTACGGGCGGCGGCTGCAAGGACATGGGCTATTAAGATATTTT 792
OY 731 TACTCTAGCAAGAAATAGTGGATGACAGCGGATCCACAGCTTTATGAATGAACACA 790
DB 793 TACTCTAGCAAGAAATAGTGGATGACAGCGGATCCACAGCTTTATGAATGAACACA 852
OY 791 AGTGGCGCAATGTGATATCTATTAAGAAAGCTGACACAGTATGCTGTTCTTCAAAA 850
DB 853 AGTGGCGCAATGTGATATCTATTAAGAAAGCTGACACAGTATGCTGTTCTTCAAAA 912
OY 851 GCAGTGTGTTCTTACGCTGATATACCTGCGGCGGCTGCAACTGAACTCAAGCCGACAGC 910
DB 913 GCAGTGTGTTCTTACGCTGATATACCTGCGGCGGCTGCAACTGAACTCAAGCCGACAGC 972
OY 911 AGATCTGTGGCGGAGGAGAGCGCGCTCCCGGCGGCTGAGGAGGAGTCAAGCTTCA 970
DB 973 AGATCTGTGGCGGAGGAGAGCGCGCTCCCGGCGGCTGAGGAGGAGTCAAGCTTCA 1031
OY 971 GGTCCAGAACGTCACAGTGTGGGAGGCTCCATCATCACCCCGAGTGGATCTGACAGC 1030
DB 1032 GGTCCAGAACGTCACAGTGTGGGAGGCTCCATCATCACCCCGAGTGGATCTGACAGC 1091
OY 1031 CGCCACAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 1090
DB 1092 CGCCACAGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAT 1151
OY 1091 TTTGAGCAATCTTCTCATGTTCTATGAGCCGAGTACCAAGTGAAGAAAGATTTCTCA 1150
DB 1152 TTTGAGCAATCTTCTCATGTTCTATGAGCCGAGTACCAAGTGAAGAAAGATTTCTCA 1211
OY 1151 TCCAAATTTATGACTCCAGACCAAGCAATGACATTCGCTGATGAAGCTGACAGAACCC 1210
DB 1212 TCCAAATTTATGACTCCAGACCAAGCAATGACATTCGCTGATGAAGCTGACAGAACCC 1271
OY 1211 TCTGACTTTCAGACGACCTGATGAAACAGTGTGTGCTGCCAACCGAGCATGATCTCA 1270
DB 1272 TCTGACTTTCAGACGACCTGATGAAACAGTGTGTGCTGCCAACCGAGCATGATCTCA 1331
OY 1271 GCCAGAACAGCTCTCTGATTTCCGGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGCTC 1330
DB 1332 GCCAGAACAGCTCTCTGATTTCCGGGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGCTC 1391
OY 1331 AGAAGTGTGAACGCTGACAGGCTCTTCTCATTTGAGACAGAGATGCAACAGCAGATA 1390
DB 1392 AGAAGTGTGAACGCTGACAGGCTCTTCTCATTTGAGACAGAGATGCAACAGCAGATA 1451
OY 1391 TGTCTATGACAACTGATACACACAGCCATGATCTGTCCGGCTTCTGTCAGGAGGAACT 1450
DB 1452 TGTCTATGACAACTGATACACACAGCCATGATCTGTCCGGCTTCTGTCAGGAGGAACT 1511
OY 1451 CGATCTTGCCAGGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1510
DB 1512 CGATCTTGCCAGGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 1571
OY 1511 GCTGATAGGAGATACAACTGGGAGTGTGCTGTGCTCCAAAGCTTACAGACAGAGAGTGA 1570
DB 1572 GCTGATAGGAGATACAACTGGGAGTGTGCTGTGCTCCAAAGCTTACAGACAGAGAGTGA 1631
OY 1571 CGGGAATGTGATGATTCAGAGGAGTGTGATTTATGCAAAATGAGGAGCAGCGCTAATC 1630
DB 1632 CGGGAATGTGATGATTCAGAGGAGTGTGATTTATGCAAAATGAGGAGCAGCGCTAATC 1691
OY 1631 CACATGATCTTGCTGCTGATGAGTGTGTTTACAAAGAAACATGAGGAGGAGTGTGCTCC 1690
DB 1632 CACATGATCTTGCTGCTGATGAGTGTGTTTACAAAGAAACATGAGGAGGAGTGTGCTCC 1751
OY 1631 CCGTCATGATTTACTCTTAAGATGATTCAGAGGCTCACTTATTTTAAACAGTGA 1750
DB 1752 CCGTCATGATTTACTCTTAAGATGATTCAGAGGCTCACTTATTTTAAACAGTGA 1811
OY 1751 ACTTGTCTGGCTTTGGCACTCTCTGCAATTTCTGTGACAGGCTGCAAGTCCCTGCCCA 1810
DB 1812 ACTTGTCTGGCTTTGGCACTCTCTGCAATTTCTGTGACAGGCTGCAAGTCCCTGCCCA 1871

[illegible]

QY	2890	GGTCCAGGANTGAAAGTAATGATTCACAGCTAGAGACTTAACCTTGAATGAAAGTCT	2949
QY	2948	GTTTCACGAAGTAAGTAATGATTCACAGCTAGAGACTTAACCTTGAATGAAAGTCT	3007
QY	2950	TGCATATCCCATTTTCAGAGATCCGCTGTGACATGACCTCTGTAGAGAGAGCATTTCCAG	3009
Db	3008	TGCATATCCCATTTTCAGAGATCCGCTGTGACATGACCTCTGTAGAGAGAGCATTTCCAG	3067
QY	3010	GGACCTTGGAAACAGTTGGCACGTGAAGGTGCTTGCCTCCCAAGACACATCTTAAAGGT	3069
Db	3068	GGACCTTGGAAACAGTTGGCACGTGAAGGTGCTTGCCTCCCAAGACACATCTTAAAGGT	3127
QY	3070	GTTTGAATGGGAAAGAGCTCTCTCTCTTTATTTAGTCCCTCTTATTTATGTAACACTG	3129
Db	3128	GTTTGAATGGGAAAGAGCTCTCTCTCTTTATTTAGTCCCTCTTATTTATGTAACACTG	3187
QY	3130	TTTGCTTTTCTTTTGTATCTTTTAAACGTGAAGTCAATGTGAAATGAATATCATG	3189
Db	3168	TTTGCTTTTCTTTTGTATCTTTTAAACGTGAAGTCAATGTGAAATGAATATCATG	3247
QY	3190	CAATTAATTAATATGCGATTTTCTTTCACAAAGTAACACATGCATCTTGAAGTTCGCTCG	3249
Db	3248	CAATTAATTAATATGCGATTTTCTTTCACAAAGTAACACATGCATCTTGAAGTTCGCTCG	3307
QY	3250	TGAGTAGAGACCAAGCTCCATTTCTTTATTAAGGGGTATATGTAGAGCTGTGTCAGAG	3309
Db	3308	TGAGTAGAGACCAAGCTCCATTTCTTTATTAAGGGGTATATGTAGAGCTGTGTCAGAG	3367
QY	3310	ACCAATAGGTGAGGACGAGCCAGACTGTGTCTCTCTGTTGGTGGCCCTCAGTTCCTGCA	3369
Db	3368	ACCAATAGGTGAGGACGAGCCAGACTGTGTCTCTCTGTTGGTGGCCCTCAGTTCCTGCA	3426
QY	3370	GCTGTCTCTTGTGAGAGAGTCCCAATGACATCTTCTATTAATTTCTTAATAGTCTG	3426
Db	3427	GCTGTCTCTTGTGAGAGAGTCCCAATGACATCTTCTATTAATTTCTTAATAGTCTG	3483
RESULT 6			
ABV27589			
ID	ABV27589	standard; cDNA; 3483 BP.	
XX	AC	ABV27589;	
XX	DT	16-SEP-2002 (first entry)	
XX	DE	Human prostate expression marker cDNA 27580.	
XX	XX	Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;	
XX	KM	Pharmacogenomic marker; gene; ss.	
OS	XX	Homo sapiens.	
PN	XX	W0200160860-A2.	
PD	XX	23-AUG-2001.	
PF	XX	20-FEB-2001; 2001WO-US05171.	
PR	XX	17-FEB-2000; 2000US-183319P.	
PR	XX	16-MAR-2000; 2000US-189862P.	
PR	XX	25-MAY-2000; 2000US-207454P.	
PR	XX	09-JUN-2000; 2000US-211314P.	
PR	XX	18-JUL-2000; 2000US-219007P.	
PR	XX	13-DEC-2000; 2000US-255281P.	
PA	XX	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.	
PI	XX	Schlegel R, Endege WO, Monahan JE;	
DR	XX	WPI; 2001-662795/76.	
PT	XX	Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful	

PT for detecting presence of prostate cancer, stage of prostate cancer
XX
PS Claim 1; Page 5642-5643; 11750bp; English.
XX
CC The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (I) is also useful as a pharmacodynamic or pharmacogenomic marker.
XX
SQ Sequence 3483 BP; 801 A; 860 C; 938 G; 884 T; 0 other:

Query Match 96.8%; Score 3331.8; DB 23; Length 3483;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3403; Conservative 0; Mismatches 7; Indels 7; Gaps 6;

QY 11 GGCCTAGTAGGCGGAGCTTAAGCAGAGGCGGAGGCGGAGGCGGAGGCGGAGG 70
DB 73 GGTGATAGAGGCGGAGCTTAAGCAGAGGCGGAGGCGGAGGCGGAGGCGGAGG 132
QY 71 AGCGCGCGCTGGAGCGGCGGAGCTATTTGAACATTCACATTCATTCATTCGAT 130
DB 133 AGCGCGCGCTGGAGGCGGAGCTATTTGAACATTCACATTCATTCATTCGAT 192
QY 131 GCTGTGATTAACAGCAAGATGGCTTGAACACAGGCTCACACCGCATTTGGAGCTAC 190
DB 193 GCTGTGATTAACAGCAAGATGGCTTGAACACAGGCTCACACCGCATTTGGAGCTAC 252
QY 191 TATGAAACCATGATATACCAACCGGAAACCCCTATCCCGACAGCCCATCTGTGCC 250
DB 253 TATGAAACCATGATATACCAACCGGAAACCCCTATCCCGACAGCCCATCTGTGCC 312
QY 251 ACTGCTTACGAGAGTGCATCCGGCTCAGTACTACCCGTCGCCGCTCCCAAGTACGCC 310
DB 313 ACTGCTTACGAGAGTGCATCCGGCTCAGTACTACCCGTCGCCGCTCCCAAGTACGCC 372
QY 311 AGGGCTCAGAGGAGGCTTCCAAACCCGTCGTCGACAGGCGCAATCCCATCCGG 370
DB 373 AGGGCTCAGAGGAGGCTTCCAAACCCGTCGTCGACAGGCGCAATCCCATCCGG 432
QY 371 ACAGTGTGCACCTCAAAAGACTAAGAAAGCAGTGTGCATCACCCTTGGGGAGCTTC 430
DB 433 ACAGTGTGCACCTCAAAAGACTAAGAAAGCAGTGTGCATCACCCTTGGGGAGCTTC 492
QY 431 CTCGTGGAGAGCTGCGCTGGCGCTGCTACTCTGGAAGTTCATGGGACAGCAAGTCTCC 490
DB 493 CTCGTGGAGAGCTGCGCTGGCGCTGCTACTCTGGAAGTTCATGGGACAGCAAGTCTCC 552
QY 491 AACCTGGGATAGAGTGGAGCTCCTCAGGTACCTGATCAACCCCTTAACTGGGTAT 550
DB 553 AACCTGGGATAGAGTGGAGCTCCTCAGGTACCTGATCAACCCCTTAACTGGGTAT 612
QY 551 GCGGTGTACACATGCGCGCGGAGGAGAGCAAGATCGGTGTGTGCGCTCTACAGCA 610
DB 613 GCGGTGTACACATGCGCGCGGAGGAGAGCAAGATCGGTGTGTGCGCTCTACAGCA 672
QY 611 AACCTCATCTTCAAGGTACTCATCTCAGAGAAAGTCTTGCCACCTGTGTGCAAGAC 670
DB 673 AACCTCATCTTCAAGGTACTCATCTCAGAGAAAGTCTTGCCACCTGTGTGCAAGAC 732
QY 671 GACTGGAACGAACTAGGGGCGGGGCGCTGCAAGGACATGGGCTATAAAGAAATTTT 730
DB 733 GACTGGAACGAACTAGGGGCGGGGCGCTGCAAGGACATGGGCTATAAAGAAATTTT 792

QY 731 TACTCTAGCCAAAGAAATAGTGATGACAGCGGATCCACACCTTTATGAACATGAACACA 790
DB 733 TACTCTAGCCAAAGAAATAGTGATGACAGCGGATCCACACCTTTATGAACATGAACACA 852
QY 791 AGTGGCGGCAATGTGATATCTATATAAAAGCTATACACAGTATGCTGTCTTCAAAA 850
DB 853 AGTGGCGGCAATGTGATATCTATATAAAAGCTATACACAGTATGCTGTCTTCAAAA 912
QY 851 GCAGTGTCTTCTTACGCTGTATACCTGCGGGGCTCAACTGAAGCTCAAGCGCGACAGC 910
DB 913 GCAGTGTCTTCTTACGCTGTATACCTGCGGGGCTCAACTGAAGCTCAAGCGCGACAGC 972
QY 911 AGGATCGTGGGCGGAGAGCGCGCTCCCGGGGCGCTGCGCTGGGAGCTCAGCTTCA 970
DB 973 AGGATGTGGGCGGAGAGCGCGCTCCCGGGGCGCTGCGCTGCGCTGCGCTGCGCTCA 1031
QY 971 CGTCCAGAAAGCTCCACGCTGCGGAGGCTCCATCATCACCCCGAGTGTGATGACAGC 1030
DB 1032 CGTCCAGAAAGCTCCACGCTGCGGAGGCTCCATCATCACCCCGAGTGTGATGACAGC 1091
QY 1031 CGCCCACTGCGTGGAAAAACCTTAAACATTCATGAGGATTTGGGGGAT 1090
DB 1032 CGCCCACTGCGTGGAAAAACCTTAAACATTCATGAGGATTTGGGGGAT 1151
QY 1091 TTTGAGACAATCTTTCATGTTCTATGAGCCGATATCCAGTAGAAAAAGTATTTCTCA 1150
DB 1152 TTTGAGACAATCTTTCATGTTCTATGAGCCGATATCCAGTAGAAAAAGTATTTCTCA 1211
QY 1151 TTCAATTTATGACTCCAAAGACCAAGACATATACATTCGCTGATGAAGCTGACAGACC 1210
DB 1212 TTCAATTTATGACTCCAAAGACCAAGACATATACATTCGCTGATGAAGCTGACAGACC 1271
QY 1211 TCTGACTTTCAACGACATAGTGAACCAAGTGTGTGCGCAACCGCATGATGCTGCA 1270
DB 1272 TCTGACTTTCAACGACATAGTGAACCAAGTGTGTGCGCAACCGCATGATGCTGCA 1331
QY 1271 GCCAGAACAGCTCTGCTGATTTCCGGGTGGGGGCCACCGAGAGAAAGGAGACCTC 1330
DB 1332 GCCAGAACAGCTCTGCTGATTTCCGGGTGGGGGCCACCGAGAGAAAGGAGACCTC 1391
QY 1331 AGAAGTGTGAACGCTGCCAAGGTGCTCTCATTTGAGACACAGAGATGCAACAGCATTA 1390
DB 1392 AGAAGTGTGAACGCTGCCAAGGTGCTCTCATTTGAGACACAGAGATGCAACAGCATTA 1451
QY 1391 TGTCTATGACAACCTGATACACACCGCATATGTCGCGGCTTCTGCGAGGGGAAGT 1450
DB 1452 TGTCTATGACAACCTGATACACACCGCATATGTCGCGGCTTCTGCGAGGGGAAGT 1511
QY 1451 CGATTCCTTGCAGAGGTGACAGTGAAGGCGCTGTGCTCACTTCAAGAAACATATTCGCTG 1510
DB 1512 CGATTCCTTGCAGAGGTGACAGTGAAGGCGCTGTGCTCACTTCAAGAAACATATTCGCTG 1571
QY 1511 GCTGATAGGGATATACAGCTGGGGTGTGCTGTGCTGCTCAAGACTTACAGACAGAGTGA 1570
DB 1572 GCTGATAGGGATATACAGCTGGGGTGTGCTGTGCTGCTCAAGACTTACAGACAGAGTGA 1631
QY 1571 CGGGAATGATGATGATATACGGAAGTATGATTAATGCAAAATGAGGGGAGAGCGGTATC 1630
DB 1632 CGGGAATGATGATGATATACGGAAGTATGATTAATGCAAAATGAGGGGAGAGCGGTATC 1691
QY 1631 CACATGCTCTTCTGCTTACAGCTGCTTTTACAGAAAAACAATGGGCGTGTGTTGCTTCC 1690
DB 1692 CACATGCTCTTCTGCTTACAGCTGCTTTTACAGAAAAACAATGGGCGTGTGTTGCTTCC 1751
QY 1691 CCGTGCATGATTTACTCTTAAAGATGATTCAGAGTCACTTCAATTTTATTAACAGTGA 1750
DB 1752 CCGTGCATGATTTACTCTTAAAGATGATTCAGAGTCACTTCAATTTTATTAACAGTGA 1811
QY 1751 ACTTGTCTGCTTGGGCACTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1810
DB 1812 ACTTGTCTGCTTGGGCACTCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1871

Qy	1811	GCCTGCTCCCTACACCCCTTTCGCGCAAGGGGTATGGCGGGTGGTGTGGGACATCG	1870
Db	1872	GCCCTGCTCTCCCTAACCCCTTGTCTCCCAAGGGGTATGGCGGGTGTGGGACATCG	1931
Qy	1871	CGCTCAAGTGTGAGAGAGAGGGGTGAGAGCTGGCCCATTTGAGATCTTCCCTGGCTAGCT	1930
Db	1932	CGGTCAAGTGTGGAGAGAGGGGTGAGAGCTGGCCCATTTGAGATCTTCCCTGGTATGCT	1991
Qy	1931	TTCCAGGGGCCAATTTTGGATGAGCATTGAAGCTGTACCTCTACCTGCTGGATGACATWG	1990
Db	1992	TTCCAGGGGCCAATTTTGGATGAGCATTGAAGCTGTACCTCTACCTGCTGGATGACATWG	2051
Qy	1991	AGATGAAAAAGGAGAGACATGGAABAAGGAGACACCGAGTGGCACCTGCAGGGCTG-CC	2049
Db	2052	AGATGAAAAAGGAGAGACATGGAABAAGGAGACACCGAGTGGCACCTGCAGGGCTGCCC	2111
Qy	2050	TTCTGGGGCCACTTGTGTGTGTCCCGACCTCTCCACAGGGGATTTTGTCTGATGGG	2109
Db	2112	TTCTGGGGCCACTTGTGTGTGTCCCGACCTCTCTCCACAGGGGATTTTGTCTGATGGG	2171
Qy	2110	TTCTTACAGCCTTACGACGCCCTGGATGGTGGCCAGAAATTAAGGAGACAGCCCTTCATGG	2169
Db	2172	TTCTTACAGCCTTACGACGCCCTGGATGGTGGCCAGAAATTAAGGAGACAGCCCTTCATGG	2231
Qy	2170	GTGGTGAACGTGTGTATGTACTTGTAAAGGGGAACAGAAATTTTGTCTTATGGGGTGA	2229
Db	2232	GTGGTGAACGTGTGTATGTACTTGTAAAGGGGAACAGAAATTTTGTCTTATGGGGTGA	2290
Qy	2230	GAATATATGACAGTGGCCCTTGGGTGGCAGAGGAAGCAATTAAGAAAGAACCTTGGCCGTGACA	2289
Db	2291	GAATATATGACAGTGGCCCTTGGGTGGCAGAGGAAGCAATTAAGAAAGAACCTTGGCCGTGACA	2349
Qy	2290	CTCTGGTGGAGGTCTTCACCTTGACACATTTGGGTGGGCTCTGGAGGAGAGACATCAGCT	2349
Db	2350	CTCTGGTGGAGGTCTTCACCTTGACACATTTGGGTGGGCTCTGGAGGAGAGACATCAGCT	2409
Qy	2350	TTCTCTCTCATCTCTCCCTGACACCTGCTGCTCTAGACACCTGGAGAGTGCACATGCCCTTGT	2409
Db	2410	TTCTCTCTCATCTCTCCCTGACACCTGCTGCTCTAGACACCTGGAGAGTGCACATGCCCTTGT	2469
Qy	2410	CTCTGGGAGGGGGCCCAAGTCTGGACACCAATTTGGGCTCTTACAGGCTGTGTACATCGG	2469
Db	2470	CTCTGG--CAGGGGCCCAAGTCTGGACACCAATTTGGGCTCTTACAGGCTGTGTACATCGG	2527
Qy	2470	AAATTTGAGGTCCATGGGGGAAATCAAGGATGTCTCACTTAAAGTACACATGTTTCCATGTT	2529
Db	2528	AAATTTGAGGTCCATGGGGGAAATCAAGGATGTCTCACTTAAAGTACACATGTTTCCATGTT	2587
Qy	2530	ATGTTTCTACACATGTCTTACTCTAGTGTCTGTGGAAACTTGTGATGTCTCAAGT	2589
Db	2588	ATGTTTCTACACATGTCTTACTCTAGTGTCTGTGGAAACTTGTGATGTCTCAAGT	2647
Qy	2590	AGTCCACCTTCATTTAACTTTTGAACAGTATCATCTTTGGCAAGTAAAGTGGTGGCC	2649
Db	2648	AGTCCACCTTCATTTAACTTTTGAACAGTATCATCTTTGGCAAGTAAAGTGGTGGCC	2707
Qy	2650	TATTTACGCTCTTTGACAAATGACTGGCTCTGTACTTTAACTTCTATTAATGAATGTG	2709
Db	2708	TATTTACGCTCTTTGACAAATGACTGGCTCTGTACTTTAACTTCTATTAATGAATGTG	2767
Qy	2710	CTGAGAGCAAAAGTCCCATGTGTGGCGGCGAAGAAAGAAAGATGTGTTTGTGGACTC	2768
Db	2768	CTGAGAGCAAAAGTCCCATGTGTGGCGGCGAAGAAAGAAAGATGTGTTTGTGGACTC	2827
Qy	2770	TTCTGTGCTCCCTTCACATGTGTGGGTTCACACAGGGGAAGGGCTCTTTGATGATGC	2829
Db	2828	TTCTGTGCTCCCTTCACATGTGTGGGTTCACACAGGGGAAGGGCTCTTTGATGATGC	2887
Qy	2830	CAAGTGGCATTAACCATGAGCATTCTTACATGTTCTGCCCTCTGGCACAAGCAGCTG	2889
Db	2888	CAAGTGGCATTAACCATGAGCATTCTTACATGTTCTGCCCTCTGGCACAAGCAGCTG	2947
Qy	2890	GTTTTGCAGATGAATGAATGATTTCTACAGCTAGACATTAACTTGAATGAAAATGCT	2949

Db	2948	GTTCACAGAATGAAATGAATGATTCACAGCTAGACTTAACCTTGAATGGAAGTCT	3007
QY	2950	TGCATATCCATTTTGCAGATCCGTCGTGCACATGCCCTGTAGAGACAGCATTTCCAG	3009
Db	3008	TGCATATCCATTTTGCAGATCCGTCGTGCACATGCCCTGTAGAGAGACAGCATTTCCAG	3067
QY	3010	GGACCTTGGAAACAGTTGGCACTGTAGGTGCTTCTCCCAAGACACATCTAAAGGT	3069
Db	3068	GGACCTTGGAAACAGTTGGCACTGTAGGTGCTTCTCCCAAGACACATCTAAAGGT	3127
QY	3070	GTTGTAATGGGAAAGCTCTCTCTTATATGCCCCCTCTATATGTGAACACTG	3129
Db	3128	GTTGTAATGGGAAAGCTCTCTCTTATATGCCCCCTCTATATGTGAACACTG	3187
QY	3130	TTTTGCTTTTTTTGTATCTTTTTTAACTGTAAATCAATGTGAAATGAATTCATG	3189
Db	3188	TTTTGCTTTTTTTGTATCTTTTTTAACTGTAAATCAATGTGAAATGAATTCATG	3247
QY	3190	CAATTAATTAATGCGATTTTTTTTCAAAATGACACATGCAATCTTTGAAGTTCTGCTGG	3249
Db	3248	CAATTAATTAATGCGATTTTTTTTCAAAATGACACATGCAATCTTTGAAGTTCTGCTGG	3307
QY	3250	TGAGTAGAGACCAAGCTCCATTTCTTATTAAGGGGTGATGTTGAGGCTGTGTAGAG	3309
Db	3308	TGAGTAGAGACCAAGCTCCATTTCTTATTAAGGGGTGATGTTGAGGCTGTGTAGAG	3367
QY	3310	ACCAAGGTGAGAGCCAGAGCTTGGTCTCTGTGGTGTGCTGCCCTCAGTTCCTGCA	3369
Db	3368	ACCAAGGTGAGAGCCAGAGCTTGGTCTCTGTGGTGTGCTGCCCTCAGTTCCTGCA	3426
QY	3370	GCTGTCTCTGTTGGAGAGGTCCTCAAAATGACTCCTTATATATCTAATAGTCTG	3426
Db	3427	GCTGTCTCTGTTGGAGAGGTCCTCAAAATGACTCCTTATATATCTAATAGTCTG	3483
RESULT 7			
ABV29119	ABV29119 standard; cDNA; 3483 BP.		
XX	ABV29119;		
AC	ABV29119;		
XX	16-SEP-2002 (first entry)		
DT	16-SEP-2002 (first entry)		
XX	Human prostate expression marker cDNA 29110.		
DE	Human prostate expression marker cDNA 29110.		
XX	Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker		
KW	Human: prostate cancer; cytostatic; carcinogen; pharmacodynamic marker		
KX	pharmacogenomic marker; gene; ss.		
XX	Homo sapiens.		
XX	OS		
XX	WO200160860-A2.		
PN	23-AUG-2001.		
PD	23-AUG-2001.		
XX	20-FEB-2001; 2001WO-US05171.		
PE	20-FEB-2001; 2001WO-US05171.		
XX	17-FEB-2000; 2000US-183319P.		
PR	16-MAR-2000; 2000US-189862P.		
PR	25-MAY-2000; 2000US-207454P.		
PR	09-JUN-2000; 2000US-211314P.		
PR	18-JUL-2000; 2000US-219007P.		
PR	13-DEC-2000; 2000US-255281P.		
XX	(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.		
PA	Schlegel R, Endege WO, Monahan JE;		
P1	WPI; 2001-662795/76.		
XX	Novel isolated nucleic acid molecule associated with cancerous state of		
PT	prostate cells and correlating with presence of prostate cancer, useful		
PT	for detecting presence of prostate cancer, stage of prostate cancer -		


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Db 1872 GCTGCTCTCCCTAAACCCCTGTCCGAAAGGGGTGATGGCCGGGTGTGTGGGACTG 1931
Qy 1871 CGGTCAAGTGTGAGAGAGAGGGGTGGAGGCTGCCCATTTGAGATGCTTCCTGTGAGTCT 1930
Db 1932 CGGTCAAGTGTGAGAGAGAGGGGTGGAGGCTGCCCATTTGAGATGCTTCCTGTGAGTCT 1931
Qy 1931 TTCCAGGGGCCAAATTTTGGATGAGCATGAGAGTGTACCTCTCACTGCTGATGATG 1990
Db 1992 TTCCAGGGGCCAAATTTTGGATGAGCATGAGAGTGTACCTCTCACTGCTGATGATG 2051
Qy 1991 AGATCAAAAAGAGAGAGATGGAAGAGAGACAGCAGGAGTGGCAGCTGAGCGCTG -CC 2049
Db 2052 AGATCAAAAAGAGAGAGATGGAAGAGAGACAGCAGGAGTGGCAGCTGAGCGCTG 2111
Qy 2050 TCTGGGGCAGCTGTGATGTGTCCAGCCTACCTCTCCACAAGGGGATTTTCTGTGAG 2109
Db 2112 TCTGGGGCAGCTGTGATGTGTCCAGCCTACCTCTCCACAAGGGGATTTTCTGTGAG 2171
Qy 2110 TTCTTAGAGCCTTAGACAGCCCTGATGGTGCCAGAAATTAAGGGAGCAGCCCTCATG 2169
Db 2172 TTCTTAGAGCCTTAGACAGCCCTGATGGTGCCAGAAATTAAGGGAGCAGCCCTCATG 2231
Qy 2170 GTGGGAGGTGGTATGACCTTTGTAAGGGGAAACAAACATTTTCTTATGGGCTGA 2229
Db 2232 GTGGGAGGTGGTATGACCTTTGTAAGGGGAAACAAACATTTTCTTATGGGCTGA 2290
Qy 2230 GAATATAGACAGTGGCTTGGGTGGAGGAAAGCAATTAAGAAAGAACTTGGCCTGAGCA 2289
Db 2231 GAATATAGACAGTGGCTTGGGTGGAGGAAAGCAATTAAGAAAGAACTTGGCCTGAGCA 2349
Qy 2290 CTCTGTGGAGGTCTGCCACCTGCACATTTGGGTGGGCTCTGGAGAGGAGACTAGCCT 2349
Db 2350 CTCTGTGGAGGTCTGCCACCTGCACATTTGGGTGGGCTCTGGAGAGGAGACTAGCCT 2409
Qy 2350 TCCCTCCATCTCTCCCTACCCCTGCTCTAGACCCCTGGAAGGTGCACATGCCCCCTGT 2409
Db 2410 TCCCTCCATCTCTCCCTACCCCTGCTCTAGACCCCTGGAAGGTGCACATGCCCCCTGT 2469
Qy 2410 CCTGGGAGGGGCGCAAGTGTGAGCACCATGTGGGCTCTTTCAGGCTGCTATGACTGG 2469
Db 2470 CCTGG - -CAGGGGCGCAAGTGTGAGCACCATGTGGGCTCTTTCAGGCTGCTATGACTGG 2527
Qy 2470 AAATTTAGCTTCATGGGGGAAATCAAGATGCTCAGTTTAAGTACACTGTTTCCATGTT 2529
Db 2528 AAATTTAGCTTCATGGGGGAAATCAAGATGCTCAGTTTAAGTACACTGTTTCCATGTT 2587
Qy 2530 ATGTTTCTACACATTTGCTACCTCATGCTCTCCGAAACTTACCTTTGATGCTCCAACT 2589
Db 2588 ATGTTTCTACACATTTGCTACCTCATGCTCTCCGAAACTTACCTTTGATGCTCCAACT 2647
Qy 2590 AGTCACCTTATTTACTCTTTTGAACGTATCATCTTTGGCAAGTAAGAGTGGGCGC 2649
Db 2648 AGTCACCTTATTTACTCTTTTGAACGTATCATCTTTGGCAAGTAAGAGTGGGCGC 2707
Qy 2650 TATTTACGCTCTTGTGACAAATGACTGGCTCTGACTTAACGTTCTATAATGATGTG 2709
Db 2708 TATTTACGCTCTTGTGACAAATGACTGGCTCTGACTTAACGTTCTATAATGATGTG 2767
Qy 2710 CTGAAGCAAAATGGCCATGCTGGCGGCGCAAGAGAAAGATGTGTTTGTGACATC 2769
Db 2768 CTGAAGCAAAATGGCCATGCTGGCGGCGCAAGAGAAAGATGTGTTTGTGACATC 2827
Qy 2770 TCTGTGTCCTTCCATAGTGTGGTTTCCAAACAGGGGAAAGGCTTGTGATTCG 2829
Db 2828 TCTGTGTCCTTCCATAGTGTGGTTTCCAAACAGGGGAAAGGCTTGTGATTCG 2887
Qy 2830 CAAGTCCATTAACATGAGCACTACTACTACTACTACTACTACTACTACTACTACTACT 2889
Db 2888 CAAGTCCATTAACATGAGCACTACTACTACTACTACTACTACTACTACTACTACTACT 2947
Qy 2890 GTTTGCAAGATGAATGATATCTTACAGTACGACTTAACCTTGAATGGAAGTCT 2949
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Db 2948 GTTTGCAAGATGAATGAATGATTTCTACAGCTAGACCTTAACCTTGAATGGAAGTCT 3007
Qy 2950 TGCATCCCATTTTGGAGATCCGCTGTGTCACATGCTCTGTAGAGAGACATTTCCAG 3009
Db 3008 TGCATCCCATTTTGGAGATCCGCTGTGTCACATGCTCTGTAGAGAGACATTTCCAG 3067
Qy 3010 GGAACCTTGAACAGTTGGCAGCTGTAAAGTGTCTGCTCCCAAGACATCTTAAAGGT 3069
Db 3068 GGAACCTTGAACAGTTGGCAGCTGTAAAGTGTCTGCTCCCAAGACATCTTAAAGGT 3127
Qy 3070 GTTGTATGCTGAAAACGCTCTCTTATTTGCCCCCTCTTATTTATGTGAACAAGT 3129
Db 3128 GTTGTATGCTGAAAACGCTCTCTTATTTGCCCCCTCTTATTTATGTGAACAAGT 3187
Qy 3130 TTTGCTTTTGTGATCTTTTAACTGTAAAGTCAATGTGAATGAAATATCATG 3189
Db 3188 TTTGCTTTTGTGATCTTTTAACTGTAAAGTCAATGTGAATGAAATATCATG 3247
Qy 3190 CAAATTAATTAAGCAGTTTCTTCAAGTAACACATGCATCTTGAAGTCTGCTG 3249
Db 3248 CAAATTAATTAAGCAGTTTCTTCAAGTAACACATGCATCTTGAAGTCTGCTG 3307
Qy 3250 TGAGTAGACACAGCTTCCATTTCTTATTAAGGGGAGTGTAGGCTGCTGACAGG 3309
Db 3308 TGAGTAGACACAGCTTCCATTTCTTATTAAGGGGAGTGTAGGCTGCTGACAGG 3367
Qy 3310 ACCAAAGGTGAGGCAAGGCGACAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCA 3369
Db 3368 ACCAAAGGTGAGGCAAGGCG -GACTTGTGCTCTCTGTGTTGTTGCTTCAAGTCTGCA 3426
Qy 3370 GCCCTGCTGTTGGAGAGGTCCCTCAATGACTCTTCTTATTTATTTATTTAGCTG 3426
Db 3427 GCTGTCTGTTGGAGAGGTCCCTCAATGACTCTTCTTATTTATTTATTTAGCTG 3483

RESULT 8
ABV24651
ID ABV24651 standard; cDNA; 3483 BP.
XX
AC ABV24651;
XX
AC 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker cDNA 24642.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;
KW pharmacogenomic marker; gene; ss.
OS Homo sapiens.
XX
PN WO200160860-A2.
PD
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219077P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JB;
XX
XX WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer
XX

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PS Claim 1; Page 4687; 11750pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV2213) of the
CC specification or its complement. (I) is useful for:
CC (a) assessing whether a patient is afflicted with prostate cancer;
CC (b) monitoring the progression of prostate cancer in a patient;
CC (c) assessing the efficacy of a test compound to inhibit prostate
CC cancer in a patient;
CC (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC in a patient;
CC (e) selecting a composition for inhibiting prostate cancer in a patient;
CC (f) assessing the prostate cell carcinogenic potential of a compound;
CC (g) determining whether prostate cancer has metastasized in a patient;
CC (h) assessing the aggressiveness or indolence of prostate cancer in a
CC patient;
CC (i) is also useful as a pharmacodynamic or pharmacogenomic marker.

XX Sequence 3483 BP; 802 A; 860 C; 937 G; 884 T; 0 other;

Query Match 96.7%; Score 3330.2; DB 23; Length 3483;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3402; Conservative 0; Mismatches 8; Indels 7; Gaps 6;

QY 11 GCGCGAGTAGGCGCGAGCTAAGCAGAGCGAGCGAGCGAGGCGAGGCGGCGG 70
DB 73 GGTGAGATAGGCGGAGCTAAGCAGAGCGAGCGAGCGAGGCGAGGCGGCGG 132

QY 71 AGCGCGCGCTGGAGCGCGGAGCTCATATTGACATTCGAGATACATTCATCTCAT 130
DB 133 AGCGCGCGCTGGAGCGCGGAGCTCATATTGACATTCGAGATACATTCATCTCAT 192

QY 131 GCTGTATATACAGCAAGATGCTTTGACATCAGGCTCACCACAGCTATTGGACCTTAC 190
DB 193 GCTGTATATACAGCAAGATGCTTTGACATCAGGCTCACCACAGCTATTGGACCTTAC 252

QY 191 TATGAAACCATGATATACCAACCGAAACCCCTATCCCGACAGCCCACTGATGCTCC 250
DB 253 TATGAAACCATGATATACCAACCGAAACCCCTATCCCGACAGCCCACTGATGCTCC 312

QY 251 ACTGTCTAGAGGTGATCCGGCTCAGTACTACCGCTCCCGCTCCCGCTAGCGCCCG 310
DB 313 ACTGTCTAGAGGTGATCCGGCTCAGTACTACCGCTCCCGCTCCCGCTAGCGCCCG 372

QY 311 AGGCTCTGAGCGAGGCTTCCACCCGCTGCTGACAGCGAGCCCAATCCCATCCGG 370
DB 373 AGGCTCTGAGCGAGGCTTCCACCCGCTGCTGACAGCGAGCCCAATCCCATCCGG 432

QY 371 ACAGTGCACTCTCAAGAGCTAAGAAAGACTGTGATCATCACTTACCTGGGACCTTC 430
DB 433 ACGGTGCACTCTCAAGAGCTAAGAAAGACTGTGATCATCACTTACCTGGGACCTTC 492

QY 431 CTGCTGGAGAGCTGCGTGGCCGCTGCTACTCTGGAAGTTTCAATGGGACGAGTGTCC 490
DB 493 CTGCTGGAGAGCTGCGTGGCCGCTGCTACTCTGGAAGTTTCAATGGGACGAGTGTCC 552

QY 491 AACCTGGAGTAAAGTGCAGTCTCTCAGTACCTGATCAACCCCTCTAACTGGTGTAT 550
DB 553 AACCTGGAGTAAAGTGCAGTCTCTCAGTACCTGATCAACCCCTCTAACTGGTGTAT 612

QY 551 GCGGTGCACTGCGCGCGGCGGAGAGAGAGAGTGGTGTGCTGCTTACGAGACA 610
DB 613 GCGGTGCACTGCGCGCGGCGGAGAGAGAGAGTGGTGTGCTGCTTACGAGACA 672

QY 611 AACCTCATCTTCAAGTGTACTCTCAAGAGAGTCTTGGACCCCTGTGTGCAAGAC 670
DB 673 AACCTCATCTTCAAGTGTACTCTCAAGAGAGTCTTGGACCCCTGTGTGCAAGAC 732

QY 671 GACTGGAACGAGAACTACGGGCGGCGGCTGCAAGGACATGGCTATAGAAATATTTT 730
DB 733 GACTGGAACGAGAACTACGGGCGGCGGCTGCAAGGACATGGCTATAGAAATATTTT 792

QY 731 TACTCTACCAAGAGATAGTGTATGACAGGCGATCCACACCTTTATGAAGTCAACCA 790

DB 793 TACTCTACCAAGAGATAGTGTATGACAGGCGATCCACACCTTTATGAAGTCAACCA 852

QY 791 AGTGGCGGCAATGTGAT 850
DB 853 AGTGGCGGCAATGTGAT 912

QY 851 GCAGTGTCTTCTTACAGTGTATAGCCCTGGGGGCAACCTTGAAGTCAAGCGGCAAGC 910
DB 913 GCAGTGTCTTCTTACAGTGTATAGCCCTGGGGGCAACCTTGAAGTCAAGCGGCAAGC 972

QY 911 AGGATGCGGCGGCGAGAGCGGCTCCCGGGGCGCTGGCCCTGGGAGTCACTTCA 970
DB 973 AGGATGCGGCGGCGAGAGCGGCTCCCGGGGCGCTGGCCCTGGGAGTCACTTCA 1031

QY 971 GGTCCAGAGCTCCACGCTGTGCGGAGGCTCATCATCAACCCCGAGTGTGTACAGC 1030
DB 1032 GGTCCAGAGCTCCACGCTGTGCGGAGGCTCATCATCAACCCCGAGTGTGTACAGC 1091

QY 1031 CGCCCACTGCGTGGAAAAACCTTTAACATCCATGCGATTTGAGCGCATTTGGGGGAT 1090
DB 1092 CGCCCACTGCGTGGAAAAACCTTTAACATCCATGCGATTTGAGCGCATTTGGGGGAT 1151

QY 1091 TTTGAGACAATCTTTCATGTTCTATGAGCGCGATATACAGTAAAGATATTTTCA 1150
DB 1152 TTTGAGACAATCTTTCATGTTCTATGAGCGCGATATACAGTAAAGATATTTTCA 1211

QY 1151 TCCAATATATGATCTTCAAGACCAAGAACATGACATTTGCTGATGAAAGTCAAGACC 1210
DB 1212 TCCAATATATGATCTTCAAGACCAAGAACATGACATTTGCTGATGAAAGTCAAGACC 1271

QY 1211 TCTGACTTTCACAGCACTTACGAAACCAAGTGTCTGCGCCCAACCAAGCATGATGCTCA 1270
DB 1272 TCTGACTTTCACAGCACTTACGAAACCAAGTGTCTGCGCCCAACCAAGCATGATGCTCA 1331

QY 1271 GCCAGAACAGCTGTCTGATGTTTCCGGGTGGGGGCCACCGAGAGAAAGGAAGACCTC 1330
DB 1332 GCCAGAACAGCTGTCTGATGTTTCCGGGTGGGGGCCACCGAGAGAAAGGAAGACCTC 1391

QY 1331 AGAAGTGTGAACGCTGCGCAAGAGTGTCTTCTATGAGACAGAGATGCAACAGCATTA 1390
DB 1392 AGAAGTGTGAACGCTGCGCAAGAGTGTCTTCTATGAGACAGAGATGCAACAGCATTA 1451

QY 1391 TGTCTATGACAACCTGATCAACCAAGCATGATGTCGCGGCTTCTGCAAGGGAACGT 1450
DB 1452 TGTCTATGACAACCTGATCAACCAAGCATGATGTCGCGGCTTCTGCAAGGGAACGT 1511

QY 1451 CGATTCTTCCAGGAGTGAACAGTGAAGGCGCTGCTGCTCACTTCAAGAAACATATCTGGTG 1510
DB 1512 CGATTCTTCCAGGAGTGAACAGTGAAGGCGCTGCTGCTCACTTCAAGAAACATATCTGGTG 1571

QY 1511 GCTGATAGGAGATCAACAGTGGGCTTGTGCTGTGCCAAAGCTTACAGACGAGAGTGA 1570
DB 1572 GCTGATAGGAGATCAACAGTGGGCTTGTGCTGTGCCAAAGCTTACAGACGAGAGTGA 1631

QY 1571 CGGGAATGTGATGATATCAAGCAAGCACTGATTTATTCGAATAAGGCGACGCTAATC 1630
DB 1632 CGGGAATGTGATGATATCAAGCAAGCACTGATTTATTCGAATAAGGCGACGCTAATC 1691

QY 1631 CACATGCTCTGCTGCTTGAAGTGTGATTTTACAGAAACATAGGGGCTGTTTGTCTCC 1690
DB 1692 CACATGCTCTGCTGCTTGAAGTGTGATTTTACAGAAACATAGGGGCTGTTTGTCTCC 1751

QY 1691 CCGTGCATGATTTACTCTTAAAGATGATTCAGAGGTCACTTCAATTTTATTAACAGTGA 1750
DB 1752 CCGTGCATGATTTACTCTTAAAGATGATTCAGAGGTCACTTCAATTTTATTAACAGTGA 1811

QY 1751 ACTTGTCTGCTTGGCACTCTTCCCATTTCTGTGCAAGGCTGCAAGTGTCTCCCTGCCA 1810
DB 1812 ACTTGTCTGCTTGGCACTCTTCCCATTTCTGTGCAAGGCTGCAAGTGTCTCCCTGCCA 1871

QY 1811 GCTGCTCTCTCCCTTAACCCCTTGTCCGCAAGGAGTGTGATGCGGCTGTGGGACACTGG 1870

Db 1872 GCTCTCTCCCTTAACCCCTGTGCGCAAGGGGTGATGCGCGGCTGGTGTGGGCACTGG 1931
Qy 1871 CGGTCAAGTGTGGAGAGAGGGGTGGAGGCTGCCCATTTGAGATCTTCTGCTGAGTCTT 1930
Db 1932 CGGTCAAGTGTGGAGAGAGGGGTGGAGGCTGCCCATTTGAGATCTTCTGCTGAGTCTT 1991
Qy 1931 TTTCAAGGGGCCAATTTTGGATGAGCATGTGACCTCTCAGCTGCTGATGACTTG 1990
Db 1992 TTTCAAGGGGCCAATTTTGGATGAGCATGTGACCTCTCAGCTGCTGATGACTTG 2051
Qy 1991 AGATAAAAAGAGAGACATGGAAGAGAGACAGCAGTGGCAGCTGAGGGGCTG-CC 2049
Db 2052 AGATAAAAAGAGAGACATGGAAGAGAGACAGCAGTGGCAGCTGAGGGGCTGCGCC 2111
Qy 2050 TCTGGGGCACTTGGTAGTGTCCCGAGCTTACCTCTCCACAAGGGGATTTGCTGATGG 2109
Db 2112 TCTGGGGCACTTGGTAGTGTCCCGAGCTTACCTCTCCACAAGGGGATTTGCTGATGG 2171
Qy 2110 TTTTGAAGACCTTACAGACCCCTGATGTGGCCAGAAATPAAAGGACAGCCCTTCATGG 2169
Db 2172 TTTTGAAGACCTTACAGACCCCTGATGTGGCCAGAAATPAAAGGACAGCCCTTCATGG 2231
Qy 2170 GTGGAGAGTGTAGTACCTCTGTAAGGGAGACAGAAATTTTGTCTTATGAGGTGA 2229
Db 2232 GTGGAGAGTGTAGTACCTCTGTAAGGGAGACAGAAATTTTGTCTTATGAGGTGA 2290
Qy 2230 GAATATAGACAGTGCCTTGGGTGGAGAGAGCAATTTGAAAAAGAACTTGCCTGAGCA 2289
Db 2291 GAATATAGACAGTGCCTTGGGTGGAGAGAGCAATTTGAAAAAGAACTTGCCTGAGCA 2349
Qy 2290 CTCTGTGTGACAGTGTCCACCTGACACATTTGGGTGGGCTCTGGAGAGGAGACTAGCTT 2349
Db 2350 CTCTGTGTGACAGTGTCCACCTGACACATTTGGGTGGGCTCTGGAGAGGAGACTAGCTT 2409
Qy 2350 TCTCTCTATCTCTCCCTGACCTCTGCTCCAGACCCCTGAGAGTGTACATGCCCCCTTGGT 2409.
Db 2410 TCTCTCTATCTCTCCCTGACCTCTGCTCCAGACCCCTGAGAGTGTACATGCCCCCTTGGT 2469
Qy 2410 CTTGGGAGAGGGGCGCAAGTGTGGACACATTTGGGCTTCTGAGGCTCTGATGACTGG 2469
Db 2470 CCTGG--CAGGGGCGCAAGTGTGGACACATTTGGGCTTCTGAGGCTCTGATGACTGG 2527
Qy 2470 AAATGAGGTCCATGGGGAAATCAAGAGTGTCAAGTTAAAGTACACATGTTCCATGTT 2529
Db 2528 AAATGAGGTCCATGGGGAAATCAAGAGTGTCAAGTTAAAGTACACATGTTCCATGTT 2587
Qy 2530 ATGTTTCAACATGTGTAACCTCACTGCTGCTGGAACCTTACTTTGATGCTCCAACT 2589
Db 2588 ATGTTTCAACATGTGTAACCTCACTGCTGGAACCTTACTTTGATGCTCCAACT 2647
Qy 2590 AGTCCACCTTCAATTAACCTTTGAACATGTATCATCTTTGGCAAGTAGAGTGTGGCC 2649
Db 2648 AGTCCACCTTCAATTAACCTTTGAACATGTATCATCTTTGGCAAGTAGAGTGTGGCC 2707
Qy 2650 TATTTACAGTGTGTGACAAATGACTGCTCTGACTTAACTTATPAAATGAATGTTG 2709
Db 2708 TATTTACAGTGTGTGACAAATGACTGCTCTGACTTAACTTATPAAATGAATGTTG 2767
Qy 2710 CTGAAGCAAGTGGCCATGTTGGGCGGAGAAAGAAAGTGTGTTGTTTGGACATC 2769
Db 2768 CTGAAGCAAGTGGCCATGTTGGGCGGAGAAAGAAAGTGTGTTGTTTGGACATC 2827
Qy 2770 TCTGTGTCCCTTCCAAATGCTGTGGGTTTCCAAACAGGGGAAGGCTCCCTTTGCAATTC 2829
Db 2828 TCTGTGTCCCTTCCAAATGCTGTGGGTTTCCAAACAGGGGAAGGCTCCCTTTGCAATTC 2887
Qy 2830 CAAGTCCATTAACCATGAGCACTACTCTACATGTTGCTGCTCTGGCCAAAGCAGCTG 2889
Db 2888 CAAGTCCATTAACCATGAGCACTACTCTACATGTTGCTGCTCTGGCCAAAGCAGCTG 2947
Qy 2890 GTTTCAGAAATGAATGAATGATTTCTACAGTAGAGACTTAACTTGAATGGAAGTCT 2949
Db 2948 GTTTCAGAAATGAATGAATGATTTCTACAGTAGAGACTTAACTTGAATGGAAGTCT 3007

Qy 2950 TGCATCCCATTTGACAGATCCGCTGTGACATGCTCTGTAGAGACAGCATTCCTCCAG 3009
Db 3008 TGCATCCCATTTGACAGATCCGCTGTGACATGCTCTGTAGAGACAGCATTCCTCCAG 3067
Qy 3010 GGACCTTGGAAACAGTTTGGCACTGTAAAGTGTGCTCCCAAGACACATCTTAAAGGT 3069
Db 3068 GGACCTTGGAAACAGTTTGGCACTGTAAAGTGTGCTCCCAAGACACATCTTAAAGGT 3127
Qy 3070 GTTGTAAATGTTGAAACAGTCTCTCTTATGATGCTCTCTTATGATGATGAAACATG 3129
Db 3128 GTTGTAAATGTTGAAACAGTCTCTCTTATGATGCTCTCTTATGATGATGAAACATG 3187
Qy 3130 TTTTCTTTTGTGATCTTTTAACTGTAAAGTTCATTAATGTGAAATGATATCATG 3189
Db 3188 TTTTCTTTTGTGATCTTTTAACTGTAAAGTTCATTAATGTGAAATGATATCATG 3247
Qy 3190 CAATTAATTAATGAGATTTTAAAGTAAACACATGATCTTGAAGTCTGCTGG 3249
Db 3248 CAATTAATTAATGAGATTTTAAAGTAAACACATGATCTTGAAGTCTGCTGG 3307
Qy 3250 TGAATGAGACACGCTCCATTTCTTATTAAGGGGAGATGATGAGCTGCTGCTGAGAG 3309
Db 3308 TGAATGAGACACGCTCCATTTCTTATTAAGGGGAGATGATGAGCTGCTGCTGAGAG 3367
Qy 3310 ACCAAAGTGAAGGCAAGGCGACAGTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCA 3369
Db 3368 ACCAAAGTGAAGGCAAGGCG-GACTTGTGCTCTGCTGCTGCTGCTGCTGCTGCTGCA 3426
Qy 3370 GCTGTCTCTGTTGGAGAGTCCCTCAATGATGCTCTTATTAATGATGATGCTG 3426
Db 3427 GCTGTCTCTGTTGGAGAGTCCCTCAATGATGCTCTTATTAATGATGATGCTG 3483

RESULT 9
ABV29165
ID ABV29165 standard; cDNA; 3483 BP.
XX
AC ABV29165;
XX
DT 16-SEP-2002 (first entry)
XX
DE Human prostate expression marker CDNA 29156.
XX
KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker.
KW pharmacogenomic marker; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200160860-A2.
XX
PD 23-NOV-2001.
XX
PF 20-FEB-2001; 2001WO-US05171.
XX
PR 17-FEB-2000; 2000US-183319P.
PR 16-MAR-2000; 2000US-189862P.
PR 25-MAY-2000; 2000US-207454P.
PR 09-JUN-2000; 2000US-211314P.
PR 18-JUL-2000; 2000US-219007P.
PR 13-DEC-2000; 2000US-255281P.
XX
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI Schlegel R, Endege WO, Monahan JT;
XX
DR WPI; 2001-662795/76.
XX
PT Novel isolated nucleic acid molecule associated with cancerous state of
PT prostate cells and correlating with presence of prostate cancer, useful
PT for detecting presence of prostate cancer, stage of prostate cancer -
XX
PS Claim 1; Page 6204-6205; 11750pp; English.

QY	2053	GGGGCCACTTTGGTAAGTGTGTCOCCAGCCTACTCTCCACAAGGGGAGATTTTGTGATGGGTTCT	211.2
Db	2049	GGGGCCACTTTGGTAAGTGTGTCOCCAGCCTACTCTCCACAAGGGGAGATTTTGTGATGGGTTCT	210.8
QY	2113	TTAGAGCCTTAGACAGCCCTGGATGTGTGGCCAGAAATTAAGGGAGCCAGCCCTTCATGGGGTG	217.2
Db	2109	TTAGAGCCTTAGACAGCCCTGGATGTGTGGCCAGAAATTAAGGGAGCCAGCCCTTCATGGGGTG	216.8
QY	2173	GTGACGTGTAGTACCTTGTAAAGGGAAACAGAAACATTTTGTTCCTATGGGGTGAGAA	223.2
Db	2169	GTGACGTGTAGTACCTTGTAAAGGGAAACAGAAACATTTTGTTCCTATGGGGTGAGAA	222.7
QY	2233	TATTAGACAGTCCCTTTGGGTGGGAGGAGCAATTAAGAAAGAACTTGGCCCTGGAGCACTC	223.2
Db	2228	TATTAGACAGTCCCTTTGGGTGGGAGGAGCAATTAAGAAAGAACTTGGCCCTGGAGCACTC	228.6
QY	2293	CTGTGGCAGGTCTCCACACTGACATATTGGGTGGGGGTCTCCGGGAGGGAAGTACAGCCTTCC	235.2
Db	2287	CTGTGGCAGGTCTCCACACTGACATATTGGGTGGGGGTCTCCGGGAGGGAAGTACAGCCTTCC	234.6
QY	2353	TCTCATCTTCCCTGACCCCTGCTCTAGACACCTGGAGAGTGCACATGCCCTTGGTCTCT	241.2
Db	2347	TCTCATCTTCCCTGACCCCTGCTCTAGACACCTGGAGAGTGCACATGCCCTTGGTCTCT	240.6
QY	2413	GGGAGGGGGGGCCAAAGTGTGGCAACATATTGGCCCTTCAGGCCCTGCTAGTACACTGGAAA	247.2
Db	2407	GG - CAGGGGGCCAAAGTGTGGCAACATATTGGCCCTTCAGGCCCTGCTAGTACACTGGAAA	246.4
QY	2473	TTGAGGTCCATGGGGGAAATCAAGATGCTCAGTTTAAGGTTCACATGTTTCCATGTTATG	253.2
Db	2465	TTGAGGTCCATGGGGGAAATCAAGATGCTCAGTTTAAGGTTCACATGTTTCCATGTTATG	252.4
QY	2533	TTTCTACACATTCCTACCTCAGTGTCTCTGAAAACCTTAAGCTTTTGATGTCTCCAGTAAGT	259.2
Db	2525	TTTCTACACATTCCTACCTCAGTGTCTCTGAAAACCTTAAGCTTTTGATGTCTCCAGTAAGT	258.4
QY	2593	CCACCTTCATTTAACTCTTGGAAACGTATTCATCTTTGGCAAGTAAAGTGGTGCCCTAT	265.2
Db	2585	CCACCTTCATTTAACTCTTGGAAACGTATTCATCTTTGGCAAGTAAAGTGGTGCCCTAT	264.4
QY	2653	TTACAGTGTCTTACAAAATGACGTGGGCTCTGACTTAACGTTCTTAATGATGATGGTG	271.2
Db	2645	TTACAGTGTCTTACAAAATGACGTGGGCTCTGACTTAACGTTCTTAATGATGATGGTG	270.4
QY	2713	AAGCAAGTSCCATGGGTGGCGGCGAAGAAAGAAAGATGTGTTTGTGTTTGGACTCT	277.2
Db	2705	AAGCAAGTSCCATGGGTGGCGGCGAAGAAAGAAAGATGTGTTTGTGTTTGGACTCT	276.4
QY	2773	GTGGTCCCTTCCAAATGCTGTGGGTTTTCACAACAGGGGAAGGTCCTTTTGATGTTCCAA	283.2
Db	2765	GTGGTCCCTTCCAAATGCTGTGGGTTTTCACAACAGGGGAAGGTCCTTTTGATGTTCCAA	282.4
QY	2833	GTGCAATTAACCATGAGAGCACTACTCTACATGTTTGCCCTCTGGCCACAAGCAGGCTGGTT	289.2
Db	2825	GTGCAATTAACCATGAGAGCACTACTCTACATGTTTGCCCTCTGGCCACAAGCAGGCTGGTT	288.4
QY	2893	TGCAAGATGAATGAATGATTTCTACAGCTAGGACTTAACTTTGAAATGGAAGTCTTGC	295.2
Db	2885	TGCAAGATGAATGAATGATTTCTACAGCTAGGACTTAACTTTGAAATGGAAGTCTTGC	294.4
QY	2953	AATCCCAATTTGCAAGATCCGTCTGTGCACATGCTCTGTAGAGAGCAGCATTTCCAGGGA	301.2
Db	2945	AATCCCAATTTGCAAGATCCGTCTGTGCACATGCTCTGTAGAGAGCAGCATTTCCAGGGA	300.4
QY	3013	CCTTGGAAACAGTGTGGCACTGTAAAGTGTGCTGCCCAAGACACATCCTTAAGGTTGT	307.2
Db	3005	CCTTGGAAACAGTGTGGCACTGTAAAGTGTGCTGCCCAAGACACATCCTTAAGGTTGT	306.4
QY	3073	GTAATGTTGAAAAAGTCTTCTCTTATTTAGCCCTCTTATTTATGTGAACAATCTGTT	313.2
Db	3065	GTAATGTTGAAAAAGTCTTCTCTTATTTAGCCCTCTTATTTATGTGAACAATCTGTT	312.4
QY	3133	GTCCTTTTGTATCTTTTAAACGTATAAGTTCATTTGTGAAAAATGATATCATGCA	319.2

Db	3125	GTCTTTTTCGATCTTTTTCGAACTGTAAGTTCATTTGTAAGATGATATCATGC	3184
Qy	3193	ATTAATATGCGATTTTTCGAAATGA	3222
Db	3185	ATAATATATGCGATTTTTCGAAATGA	3214
RESULT 12			
AS64178	AS64178	standard; CDNA: 3245 BP.	
AC	AS64178;		
XX	29-JAN-2002	(first entry)	
XX	Human prostate CDNA sequence #597.		
XX	Human; prostate cancer; ss; cytosstatic; immunostimulant; tumour.		
XX	Homo sapiens.		
OS	WO200173032-A2.		
XX	04-OCT-2001.		
XX	27-MAR-2001; 2001WO-US09919.		
XX	27-MAR-2000; 2000US-0536857.		
XX	09-MAY-2000; 2000US-0568100.		
XX	12-MAY-2000; 2000US-0570737.		
XX	13-JUN-2000; 2000US-0593793.		
XX	27-JUN-2000; 2000US-0605783.		
XX	10-AUG-2000; 2000US-0636215.		
XX	29-AUG-2000; 2000US-0651236.		
XX	06-SEP-2000; 2000US-0651279.		
XX	02-OCT-2000; 2000US-0679426.		
XX	10-OCT-2000; 2000US-0685166.		
XX	(CORI-) CORIXA CORP.		
XX	Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;		
XX	Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;		
XX	Li SX, Wang A, Skelky YAW, Hepler WT, Henderson RA;		
XX	WPI: 2001-639232/73.		
XX	P-PSDB: AAU69960.		
XX	New human prostate-specific polypeptides and polynucleotides useful for		
XX	the diagnosis and treatment of cancer, especially prostate cancer -		
XX	Claim 1; Page 570-571; 579pp; English.		
XX	The invention relates to isolated prostate-specific		
XX	polynucleotides, polypeptides, fusion proteins of the polypeptides,		
XX	antibodies raised against the polypeptides (or antigenic epitopes		
XX	derived from them) and antigen-presenting cells expressing the		
XX	polypeptides. The antibodies are useful for detecting the presence of		
XX	cancer, especially prostate cancer. The polypeptides, polynucleotides and		
XX	the antigen-presenting cells are useful for stimulating and/or expanding		
XX	T cells specific for a tumour protein, and for inhibiting the development		
XX	of cancer especially prostate cancer. Compositions comprising the		
XX	polynucleotide and/or polypeptide are useful for stimulating an immune		
XX	response, and for treating cancer. The oligonucleotide is useful for		
XX	detecting cancer. The present sequence is a prostate specific		
XX	polynucleotide of the invention.		
XX	Sequence 3245 BP; 774 A; 818 C; 870 G; 783 T; 0 other;		
XX	Query Match	91.1%; Score 3136.8; DB 22; Length 3245;	
XX	Best Local Similarity	99.6%; Pred. No. 0;	
XX	Matches 3197; Conservative	0; Mismatches 7; Indels 6; Gaps 5;	

[illegible]

Db	1089	GAGACAACTTCAATGTTCTATGGAGCGGGATTCACAAAGTAGAAAAAGTGATTTCTCAATCC	1148
QY	1154	AAATATATACCTCCAAAGACCAAGAAACAATGACATATGGCGTGGATGAAGCTGCACAGACCTCT	1213
Db	1149	AAATATATACCTCCAAAGACCAAGAAACAATGACATATGGCGTGGATGAAGCTGCACAGACCTCT	1208
QY	1214	GACTTTCAGAGCACTAGTAGAAACCAAGTGTGTCTGCCAACCCAGGCAATGATCTGCAGACC	1273
Db	1209	GACTTTCAGAGCACTAGTAGAAACCAAGTGTGTCTGCCAACCCAGGCAATGATCTGCAGACC	1268
QY	1274	AGAACAGCTCTGCTGGATTTCCGGGTGGGGGGCCACCGAGAGGAAAGGAAAGAAAGAAAGTCTCAGA	13533
Db	1269	AGAACAGCTCTGCTGGATTTCCGGGTGGGGGGCCACCGAGAGGAAAGGAAAGGAAAGAAAGTCTCAGA	1328
QY	1334	AGTGTGAAACGCTCCCAAGGTGCTTTCATATTCAGACACAGATGCACACAGCAGATATATGT	13933
Db	1329	AGTGTGAAACGCTCCCAAGGTGCTTTCATATTCAGACACAGATGCACACAGCAGATATATGT	1388
QY	1394	CTATGACAACTGATTCACACCAAGCCATGATCTGTGCCGGCTTCTGCAGGGAGACGTGCA	14533
Db	1389	CTATGACAACTGATTCACACCAAGCCATGATCTGTGCCGGCTTCTGCAGGGAGACGTGCA	1448
QY	1454	TTCTTGGCAGGGGTACAGTGGAGGGCTCTGGTGCATCTTGGAAGAAACAATATCTGGTGGCT	15133
Db	1449	TTCTTGGCAGGGGTACAGTGGAGGGCTCTGGTGCATCTTGGAAGAAACAATATCTGGTGGCT	1508
QY	1514	GATAGGGGATPACAAGCTGGGGTTCTGGCTTGGCCAAAGCTTACAGACCAGAGTTCACG	15737
Db	1509	GATAGGGGATPACAAGCTGGGGTTCTGGCTTGGCCAAAGCTTACAGACCAGAGTTCACG	1568
QY	1574	GAATGTGATGGTATTCACGAGCTGGATTTATTCACAATAATAGGGCCAGACGGCTAATTCAC	16333
Db	1569	GAATGTGATGGTATTCACGAGCTGGATTTATTCACAATAATAGGGCCAGACGGCTAATTCAC	1628
QY	1634	ATGGCTTTCGCTCTTGACAGCTGTTTTCACAAGAAACAATAGGGGCTGGTTTGTCTTCCCG	16933
Db	1629	ATGGCTTTCGCTCTTGACAGCTGTTTTCACAAGAAACAATAGGGGCTGGTTTGTCTTCCCG	1688
QY	1694	TGCATGATTTACTCTTACAGATGATTCAGAGGTCACCTTCATTTTATTAACAGTGAAC	17533
Db	1689	TGCATGATTTACTCTTACAGATGATTCAGAGGTCACCTTCATTTTATTAACAGTGAAC	1748
QY	1734	TGCTGGCTTGGGACATCTTGCCCAATCTGTGCAAGGCTCAGTGGCTCCCTGCCACGC	18133
Db	1749	TGCTGGCTTGGGACATCTTGCCCAATCTGTGCAAGGCTCAGTGGCTCCCTGCCACGC	1808
QY	1814	TGCTCTCCCTAACCCCTTGTGCCAAGGGGTATGGCCGGCTGGTTGTGGGACATCGGGG	18737
Db	1809	TGCTCTCCCTAACCCCTTGTGCCAAGGGGTATGGCCGGCTGGTTGTGGGACATCGGGG	1868
QY	1874	TCAAGTGTGAGAGAGAGGGGTGAGAGGCTGCCCATTTGAATCTTCTGCTAGTCCCTTTC	19333
Db	1869	TCAAGTGTGAGAGAGAGGGGTGAGAGGCTGCCCATTTGAATCTTCTGCTAGTCCCTTTC	1928
QY	1934	CAGGGGCCAATTTTGGATGAGCATGGAAGTGTACCTCTCAGCTGCTGGATGACTTTGAGA	19933
Db	1929	CAGGGGCCAATTTTGGATGAGCATGGAAGTGTACCTCTCAGCTGCTGGATGACTTTGAGA	1988
QY	1994	TGAAAAAGAGAGACATGGAAGAGGAGACAGCCAGTGGCACCTGCAGCGGTG-CCTCT	20522
Db	1989	TGAAAAAGAGAGACATGGAAGAGGAGACAGCCAGTGGCACCTGCAGCGGTGCGCTCT	2048
QY	2053	GGGGGCACTTGTGTGTGCCCAAGCCACCTCTCCACAAGGGGGATTTTGTGTGATGGGTTC	21122
Db	2049	GGGGGCACTTGTGTGTGTGCCCAAGCCACCTCTCCACAAGGGGGATTTTGTGTGATGGGTTC	2108
QY	2113	TTAGAGCCTTATGACAGCCCTGGATGTGTGGCCAGAAATTAAGGAGACCAAGCCTTCATGAGGTG	21727
Db	2109	TTAGAGCCTTATGACAGCCCTGGATGTGTGGCCAGAAATTAAGGAGACCAAGCCTTCATGAGGTG	2168
QY	2173	GTGACGTGTGTACCTTGTAAAGGGGAACAGAAATTTTGTCTTATGGGGTAGAA	22322


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Db 2169 GTGACGTGGTACTCA-CCTTGTAAAGGGGAACAAACATTTTGTCTTATGGGTGAGAA 2227
Oy 2233 TATAGACAGTGGCCCTTGGTGGGAGGGAAGCAATTTGAAAAGAACTTGGCCCTGAGCACTC 2292
Db 2228 TATAGACAGTGGCCCTT-GGTGGAGGGAAGCAATTTGAAAAGAACTTGGCCCTGAGCACTC 2286
Oy 2293 CTGGTGCAGGTCTCCACCTGACATTTGGGTGGGCTCTGGAGGAGAGACTAGCCCTTCC 2352
Db 2287 CTGGTGCAGGTCTCCACCTGACATTTGGGTGGGCTCTGGAGGAGAGACTAGCCCTTCC 2346
Oy 2353 TCCCTACTCTCCCTGACCCCTGCTCCAGACCCCTGAGAGTGCATATGCCCTTGGTCTC 2412
Db 2347 TCCCTACTCTCCCTGACCCCTGCTCCAGACCCCTGAGAGTGCATATGCCCTTGGTCTC 2406
Oy 2413 GGGGAGGGGCGCCAACTGTGGCCACATGTGGCCCTTTCAGGCGCTCTAGTACTGAGAA 2472
Db 2407 GG--CAGGGCGCCAACTGTGGCCACATGTGGCCCTTTCAGGCGCTCTAGTACTGAGAA 2464
Oy 2473 TTGAGGTCCATGGGGGGAATCAAGATGCTCACTTTAAGGTACATGTTCATGTTTATG 2532
Db 2465 TTGAGGTCCATGGGGGGAATCAAGATGCTCACTTTAAGGTACATGTTCATGTTTATG 2524
Oy 2533 TTCTTACACTGTCTACCTACGTGCTCCGGAACCTTGTGTGATGCTCCAACTAGT 2592
Db 2525 TTCTTACACTGTCTACCTACGTGCTCCGGAACCTTGTGTGATGCTCCAACTAGT 2584
Oy 2593 CCACCTTCACTTAACTCTTGAACCTGTATCATCTTGGCAATAGAGTGTGGCCAT 2652
Db 2585 CCACCTTCACTTAACTCTTGAACCTGTATCATCTTGGCAATAGAGTGTGGCCAT 2644
Oy 2653 TTTCAGCTGCTTTCACAAATGACGTGCTCCGCACTTAACTTCTATTAATGAATGTGCTG 2712
Db 2645 TTTCAGCTGCTTTCACAAATGACGTGCTCCGCACTTAACTTCTATTAATGAATGTGCTG 2704
Oy 2713 AAGCAAGGCCCATGTTGGGCGGCGGAAGAAAGATGTTTGTGTGGACCTCTC 2772
Db 2705 AAGCAAGGCCCATGTTGGGCGGCGGAAGAAAGATGTTTGTGTGGACCTCTC 2764
Oy 2773 GTGGTCCCTTCCAACTGTGGGTTCCAAACAGGGGAAGGTCCTTTTGCATTTGCCAA 2832
Db 2765 GTGGTCCCTTCCAACTGTGGGTTCCAAACAGGGGAAGGTCCTTTTGCATTTGCCAA 2824
Oy 2833 GTGGCATAACCATGAGCACTACTCTACCATGTTTGTGCTCTGCGCCAAAGCAGGCTGTT 2892
Db 2825 GTGGCATAACCATGAGCACTACTCTACCATGTTTGTGCTCTGCGCCAAAGCAGGCTGTT 2884
Oy 2893 TGCAGAAATGAATGAATGATTTCTACAGTAGAGACTTAACCTTGAATGGAATGCTGTC 2952
Db 2885 TGCAGAAATGAATGAATGATTTCTACAGTAGAGACTTAACCTTGAATGGAATGCTGTC 2944
Oy 2953 AATCCATTTCAGAGATCCGCTGTGCACATGCTCTGTAGAGAGAGACTTCCAGGGA 3012
Db 2945 AATCCATTTCAGAGATCCGCTGTGTGCACATGCTCTGTAGAGAGAGACTTCCAGGGA 3004
Oy 3013 CCTTGAACACAGTTGGCACTGTAAAGTCTTGTCCCAAGACACATCTTAAAAAGTGT 3072
Db 3005 CCTTGAACACAGTTGGCACTGTAAAGTCTTGTCCCAAGACACATCTTAAAAAGTGT 3064
Oy 3073 GTPAATGGTAAAAAGCTCTCTCTTATTTAGGCCCTTCTTATTTATGTGAACAAGTGT 3132
Db 3065 GTPAATGGTAAAAAGCTCTCTCTTATTTAGGCCCTTCTTATTTATGTGAACAAGTGT 3124
Oy 3133 GTCTTTTGTGATCTTTTAACTGTAAAGTTCATATTTGAAAAATGAATATCATGCA 3192
Db 3125 GTCTTTTGTGATCTTTTAACTGTAAAGTTCATATTTGAAAAATGAATATCATGCA 3184
Oy 3193 ATTAATTAATGCAATTTTTCAAAGTAA 3222
Db 3185 ATTAATTAATGCAATTTTTCAAAGTAA 3214

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RESULT 13
AAH93942

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ID AH93942 standard; cDNA; 3245 BP.
XX
AC AH93942;
XX
DT 04-OCT-2001 (first entry)
XX
DE P100C full length cDNA sequence.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
XX cytostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001MO-US01574.
XX
PR 14-JAN-2000; 2000US-0483672.
XX
PA (COR-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Matcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAM;
PI Wang A, Meagher MJ;
XX
DR MPI; 2001-425873/45.
XX
PT New polynucleotide encoding a prostate-specific protein, for
PT diagnosing, monitoring and treating prostate cancer in a patient and
PT for use in vaccines -
XX
PS Claim 1; Page 537-538; 543pp: English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated
CC T cells prepared using (I) or (II) are used to treat cancer in a patient.
CC (I) and the antibodies are also used in the detection of cancer in a
CC patient. The cancer that is diagnosed or treated is particularly
CC prostate cancer. (I) and (II) can be used in vaccines. The antibodies or
CC (I) can be used for monitoring the progression of cancer in a patient.
CC (I) and (II) can also be used to improve diagnostic and therapeutic
CC methods for prostate cancer. They can indicate the level of metastasis
CC as well as the prostate volume. AH93357 to AH93944 and AM01115 to
CC AM01318 represent polynucleotide and amino acid sequences used in the
CC exemplification of the present invention.
XX
SQ Sequence 3245 BP; 774 A; 818 C; 870 G; 783 T; 0 other;
XX
Query Match 91.1%; Score 3136.8; DB 22; Length 3245;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3197; Conservative 0; Mismatches 7; Indels 6; Gaps 5;
Oy 14 CGAGTGGGCGCGAGCTPAGCAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 73
Db 10 CGGCTCGCGCGAGCTPAGCAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGG 69
Oy 74 GCGGCGTGGAGCGCGGAGGCTCATTTGAACATTTCCAGATACCTATCTACTGATGCT 133
Db 70 GCGGCGTGGAGCGCGGAGGCTCATTTGAACATTTCCAGATACCTATCTACTGATGCT 129
Oy 134 GTTGATPACAGCAAGATGCTTTGAAGTCAAGGTCACACACAGCTATTTGAGCTTACTAT 193
Db 130 GTTGATPACAGCAAGATGCTTTGAAGTCAAGGTCACACACAGCTATTTGAGCTTACTAT 189
Oy 194 GAATACCATGATPACCAACGGAACCCCTATTCGCGCAAGCGCACTGTGGTCCGACT 253
Db 190 GAATACCATGATPACCAACGGAACCCCTATTCGCGCAAGCGCACTGTGGTCCGACT 249
Oy 254 GTCTAGAGGTGATCCGGCTCAGTACTACCGTCCCGCTGCGCCAGTACGCCCGAGG 313

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OY 134 GTTGATTAACACCAAGATGGCTTTGAACTCAGGGTCCACCACGATATTGGACCTTACTAT 193
DB 130 GTTGATTAACACCAAGATGGCTTTGAACTCAGGGTCCACCACGATATTGGACCTTACTAT 189
OY 194 GAAACCAATGGATNCCAAACCGGAAAAACCCCTATATCCCGACAGCCACGCTGTGCCCACT 253
DB 190 GAAACCAATGGATNCCAAACCGGAAAAACCCCTATATCCCGACAGCCACGCTGTGCCCACT 249
OY 254 GTCTACGAGGTGCATCCGGCTCAGTACTACCGCTCCCGCTGACCCAGTACGCCCGGAG 313
DB 250 GTCTACGAGGTGCATCCGGCTCAGTACTACCGCTCCCGCTGACCCAGTACGCCCGGAG 309
OY 314 GTCTACGAGGTGCATCCCGCTCAGTACTACCGCTCCCGCTGACCCAGTACGCCCGGAG 373
DB 310 GTCTACGAGGTGCATCCCGCTCAGTACTACCGCTCCCGCTGACCCAGTACGCCCGGAG 369
OY 374 GTGTCCACCTCAAAAGACATCAAGAAACGATGTCATCACCCTTGGAGCCCTTCTCTC 433
DB 370 GTGTCCACCTCAAAAGACATCAAGAAACGATGTCATCACCCTTGGAGCCCTTCTCTC 429
OY 434 GTGGAGGTGCAGCTGGCGCTGAGCTTCTGGAAGTTCATGGAGGACGATGCTCCAAAC 493
DB 430 GTGGAGGTGCAGCTGGCGCTGAGCTTCTGGAAGTTCATGGAGGACGATGCTCCAAAC 489
OY 494 TCTGGGATAGAGTGCAGTCTCTCAGGTACCTGATCAACCCCTCTAAGTGTGTATGAC 553
DB 490 TCTGGGATAGAGTGCAGTCTCTCAGGTACCTGATCAACCCCTCTAAGTGTGTATGAC 549
OY 554 GTGTCCACCTCAAAAGACATCAAGAAACGATGTCATCACCCTTGGAGCCCTTCTCTC 613
DB 550 GTGTCCACCTCAAAAGACATCAAGAAACGATGTCATCACCCTTGGAGCCCTTCTCTC 609
OY 614 TTTCACTCTTCAAGTGTACTCATCTCAGAGGAAGTCTGGACCTGTGTGCCAAGACGAC 673
DB 610 TTTCACTCTTCAAGTGTACTCATCTCAGAGGAAGTCTGGACCTGTGTGCCAAGACGAC 669
OY 674 TGGAAACGAACTACGGCGCGCGCGCTGACAGGACATGGGCTATTAAGATATTTTAC 733
DB 670 TGGAAACGAACTACGGCGCGCGCGCTGACAGGACATGGGCTATTAAGATATTTTAC 729
OY 734 TCTTACCAAGGATATGATGATGACAGCGGATCCACGATTTATGAATGTAACCAAGT 793
DB 730 TCTTACCAAGGATATGATGATGACAGCGGATCCACGATTTATGAATGTAACCAAGT 789
OY 794 GCCCGCAATGTGATATCTATATAAAACCTGTACACAGTGTGCTGTCTTCAAAAGA 853
DB 790 GCCCGCAATGTGATATCTATATAAAACCTGTACACAGTGTGCTGTCTTCAAAAGA 849
OY 854 GTGGTTCTTTACGCTGTATATACCTGCGGGGTCAACTTGAAGTCAAGCCGACAGACAG 913
DB 850 GTGGTTCTTTACGCTGTATATACCTGCGGGGTCAACTTGAAGTCAAGCCGACAGACAG 909
OY 914 ATCGTGGCGGGGAGAGGGCGCTCCGGGGGCTGGCCCTGGGGGAGGTCAAGCTCAGAT 973
DB 910 ATCGTGGCGGGGAGAGGGCGCTCCGGGGGCTGGCCCTGGGGGAGGTCAAGCTCAGAT 968
OY 974 CCAGAACGTCACAGCTGTGCGGAGGCTCCATCATCACCCCGAGTGGATCGTACAGCCGC 1033
DB 969 CCAGAACGTCACAGCTGTGCGGAGGCTCCATCATCACCCCGAGTGGATCGTACAGCCGC 1028
OY 1034 CCAGTGGCTGAAAAACCTTTAACAATCATGGCATTTGAGAGCGCATTTTGGGGGATTTT 1093
DB 1029 CCAGTGGCTGAAAAACCTTTAACAATCATGGCATTTGAGAGCGCATTTTGGGGGATTTT 1088
OY 1094 GAGACAACTTTTATGTTCTATGAGCGGAGATCAACAGTAAAGAAAGATTTTCTCAACC 1153
DB 1089 GAGACAACTTTTATGTTCTATGAGCGGAGATCAACAGTAAAGAAAGATTTTCTCAACC 1148
OY 1154 AAATTTATGCTCAAGACCAAGAACATGACATTTGCTGATGAAGTGCAGAAACCTCT 1213
DB 1149 AAATTTATGCTCAAGACCAAGAACATGACATTTGCTGATGAAGTGCAGAAACCTCT 1208

OY 1214 GACTTTCAACGACCTAGTGAACCAAGTGTGTGTGCCAACCCAGGACATGATGTGCACGC 1273
DB 1209 GACTTTCAACGACCTAGTGAACCAAGTGTGTGTGCCAACCCAGGACATGATGTGCACGC 1268
OY 1274 AGAAGCTGTGTGTGATTTCCGGGTGGGGGGCCACGAGAGAAAGGAAGTCACTGAG 1333
DB 1269 AGAAGCTGTGTGTGATTTCCGGGTGGGGGGCCACGAGAGAAAGGAAGTCACTGAG 1328
OY 1334 AGTGTGAAGCTGTGCAAGGTGTCTTCTATGAGACAGAGATGACACAGATATGT 1393
DB 1329 AGTGTGAAGCTGTGCAAGGTGTCTTCTATGAGACAGAGATGACACAGATATGT 1388
OY 1394 CTATGCAACCTGATCAACACAGCCATGATGTGTCCGGTCTCGAGGGGAACGTGGA 1453
DB 1389 CTATGCAACCTGATCAACACAGCCATGATGTGTCCGGTCTCGAGGGGAACGTGGA 1448
OY 1454 TTTCTGCCAGGTTGACATGAGAGGGGCTGTGTCTTCAAGAAACATATCTGTGTGCT 1513
DB 1449 TTTCTGCCAGGTTGACATGAGAGGGGCTGTGTCTTCAAGAAACATATCTGTGTGCT 1508
OY 1514 GATAGGGATACAGAGCTGGGTTCTGGCTGTGCCAAACCTTACAGACGAGATGTAAG 1573
DB 1509 GATAGGGATACAGAGCTGGGTTCTGGCTGTGCCAAACCTTACAGACGAGATGTAAG 1568
OY 1574 GAATGTGATGTATTCACGAGTGTGATTTATGACAAATGAGGCGACAGGCTTAATCCAC 1633
DB 1569 GAATGTGATGTATTCACGAGTGTGATTTATGACAAATGAGGCGACAGGCTTAATCCAC 1628
OY 1634 ATGGCTGTGTCTGATGAGTGTGTTTACAGAAACATAGGGGCTGTGTGTGTGTGTGT 1693
DB 1629 ATGGCTGTGTCTGATGAGTGTGTTTACAGAAACATAGGGGCTGTGTGTGTGTGTGT 1688
OY 1694 TGCATGATTTACTCTTAAAGATGATTCAGAGGTCACTTATTTTATTAACAGTGAAT 1753
DB 1689 TGCATGATTTACTCTTAAAGATGATTCAGAGGTCACTTATTTTATTAACAGTGAAT 1748
OY 1754 TGTCTGGCTTTGGACCTGTGTGCCATTTGTGTACAGGCTGTGACGCTCCCTGCCACCC 1813
DB 1749 TGTCTGGCTTTGGACCTGTGTGCCATTTGTGTACAGGCTGTGACGCTCCCTGCCACCC 1808
OY 1814 TGCTCTCCCTAACCCCTTGTCCGCAAGGGGTGATGGCGGCTGTGTGGGACATGGGG 1873
DB 1809 TGCTCTCCCTAACCCCTTGTCCGCAAGGGGTGATGGCGGCTGTGTGGGACATGGGG 1868
OY 1874 TCAAGTGTGAGAGAGGGGTGTGAGGCTGCCCATTTGAGATCTTCTGCTGAGTCTTTC 1933
DB 1869 TCAAGTGTGAGAGAGGGGTGTGAGGCTGCCCATTTGAGATCTTCTGCTGAGTCTTTC 1928
OY 1934 CAGGGGCCAATTTTGTGATGAGATGAGTGTGACCTGTCAAGCTGTGATGACTTGA 1993
DB 1929 CAGGGGCCAATTTTGTGATGAGATGAGTGTGACCTGTCAAGCTGTGATGACTTGA 1988
OY 1994 TGAANAAGAGAGCATGGAAGGAGAGACAGCAGTGTGACCTGTGACCTGTGATGAG 2052
DB 1989 TGAANAAGAGAGCATGGAAGGAGAGACAGCAGTGTGACCTGTGACCTGTGATGAG 2048
OY 2053 GGGGGCACTTGTGTGTCTCCAGGCTTCTCTCCACAAGGGGATTTTGTGATGGTTTC 2112
DB 2049 GGGGGCACTTGTGTGTCTCCAGGCTTCTCTCCACAAGGGGATTTTGTGATGGTTTC 2108
OY 2113 TTAAGGCTTTACAGCCCTGTGATGTGTGCGCAGAAATTAAGGACACGCTTCAATGG 2172
DB 2109 TTAAGGCTTTACAGCCCTGTGATGTGTGCGCAGAAATTAAGGACACGCTTCAATGG 2168
OY 2173 GTAGCTGTGTGTGCTCTTGAAGGGGAACGAATTTTGTCTTATGGGGTGA 2232
DB 2169 GTAGCTGTGTGTGCTCTTGAAGGGGAACGAATTTTGTCTTATGGGGTGA 2227
OY 2233 TATAGACAGTGCCTTGGGTGTGAGGAGAAATTAAGAAAGAACTTCCCTGAGACATC 2292
DB 2228 TATAGACAGTGCCTTGGGTGTGAGGAGAAATTAAGAAAGAACTTCCCTGAGACATC 2286
OY 2293 CTGTGTGAGGTCTCCACCTGACATTTGGGTGGGGCTCTGTGGAGGAGATCAAGCTTCC 2352

513 CCTCAGGATCTGATCAACCCCTCTACCTGCTGATGCGCTGTCACACTGCCCGGCG 572
 421 CCTCAGGATCTGATCAACCCCTCTACCTGCTGATGCGCTGTCACACTGCCCGGCG 480
 573 GGGAGGAGGAGAAATGGGTGTGTGCTGCTGATGAGGACCAACTTCACTCTGAGGTACT 632
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 633 CATCTCAGAGAGATCTGCGACCTGCTGCGCAAGACACTGGAACGAGACTACGAGC 692
 541 CATCTCAGAGAGATCTGCGACCTGCTGCGCAAGACACTGGAACGAGACTACGAGC 600
 693 GGGGCGCTGCAAGGACATGGCTATAGAAATATTTTACTCTAGCCCAAGAAATAGTG 752
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 753 ATGACAGGAGATCTCAGCAGCTTATGAACTGAAACAAAGTCCGCAATGCGATATCT 812
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 900 GAGGCTCCATCATCAACCCCGAGTGTATGATGAGAGCCGCTGCTGAGAAACCT 959
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 1280 GTGCTTCTATGAGACAGAGATGCAACAGAGATATGCTATGAGAGCAACTGATCACA 1319
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 1473 GAGAGGCTCTGCTGACTTTCGAAGAAATATGCTGCTATGAGGAGATCAAGCTGAG 1532
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 1533 GGTTCGCTGCTGCAAGGCTTACAGACAGAGATGATGAGGAGATGATGATGATTCAG 1592
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1593 GACTGATTTATGACAAATGAGGCGAGAGGCTATATCCACATGCTTCTGCTTGAAG 1652
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 1860 ATGACATGAGATCTGATCACTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1919
 2010 TGGAAAGGAGAGACCGAGTGGGACCTGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2068
 1920 TGGAAAGGAGAGACCGAGTGGGACCTGCAAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1979
 2069 GTCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2128
 1980 GTCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2036
 2129 CCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2188
 2037 CCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2095
 2189 CTTGTAAGGAGAGAAATTTTGTATGAGGAGTGAATATGAGAGTCCCTT 2248
 2096 CTTGTAAGGAGAGAAATTTTGTATGAGGAGTGAATATGAGAGTCCCTT 2155
 2249 GGTGCGAGGAGAGAAATTTGAAAGAACTTCCCTGAGACACTGCTGCTGCTGCTGCTGCTGCT 2308
 2156 -GGTGGAGGAGAGAAATTTGAAAGAACTTCCCTGAGACACTGCTGCTGCTGCTGCTGCTGCTGCT 2214
 2309 CCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2368
 2215 CCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2274
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Search completed: January 15, 2003, 18:35:18
 Job time : 646 secs

Db 301 AGAAAGCACTGTGCAT

Db 301 AGAAGCACTGTGCATCACCCTTGACCCTTCCTCGTGGGAGCTGCGCTGGCG 360

OY	453	CTGGCCCTACTCGTGGAAAGTTCAATGGGGACAGCAAGTCCTCAACTCTGGGAAATGAACTGGACAT	512
Db	361	CTGGCCCTACTCTGGAAAGTTCAATGGGGACAGCAAGTCCTCAACTCTGGGAAATGAACTGGACAT	420
OY	513	CCCTAGGTACTGTGCATCAACCCCTCTAACTGGTGTGATGGCGTGTGACACATGCCCCGGCG	572
Db	421	CCTCAGGTACTGTGCATCAACCCCTCTAACTGGTGTGATGGCGTGTGACACATGCCCCGGCG	480
OY	573	GGGAGAGACAAATTCGGTGTGTGGCCCTTAAGGAACTCAACCTCAATCCTCAAGTGTACT	632
Db	481	GGGAGAGACAAATTCGGTGTGTGGCCCTTAAGGAACTCAACCTCAATCCTCAAGTGTACT	540
OY	633	CATCTCAGAGGAAGTCCTGGACCCCTGTGTGCCAAGACACTGGAACTGAACTACGGGC	692
Db	541	CATCTCAGAGGAAGTCCTGGACCCCTGTGTGCCAAGACACTGGAACTGAACTACGGGC	600
OY	693	GGGGGGCCCTGCAAGGACATGGGGCTATTAAGAAATATTTTTTACTTAGCCAAAGAAATGTGG	752
Db	601	GGGGGGCCCTGCAAGGACATGGGGCTATTAAGAAATATTTTTTACTTAGCCAAAGAAATGTGG	660
OY	753	ATGACAGCGGAATCCACCAAGCTTTATGAAACAGAAACAACTGGCCGAATGTGAAATATCT	812
Db	661	ATGACAGCGGAATCCACCAAGCTTTATGAAACAGAAACAACTGGCCGAATGTGAAATATCT	720
OY	813	ATAAAAAACTGTACACAGTGTACCGTTCCTTCAAAAAGAGTGTTTCTTTACGCTGTAA	872
Db	721	ATAAAAAACTGTACACAGTGTACCGTTCCTTCAAAAAGAGTGTTTCTTTACGCTGTAA	780
OY	873	TAGCCCTGGGGGGTCAACTGTGAACCAACACCCGCGACAGCAAGATCGTGGCGGAGAAAGG	932
Db	781	TAGCCCTGGGGGGTCAACTGTGAACCAACACCCGCGACAGCAAGATCGTGGCGGAGAAAGG	840
OY	933	CGCTTCCCGGGGGCCCTGGGCCCTGGGGCAGGTGACGCTGTGCACGTCCAGAAAGCTCACGTGTGC	992
Db	841	CGCTTCCCGGGGGCCCGTGGGCCCT - GGCAGGTGACGCTGTGCACAAAGCTCCACAGTGTGC	899
OY	993	GGAGGCTCCATATTCACCCCCGAGATGATGTGACAGCCGCCCACTGTGCTGGAAAAACT	1052
Db	900	GGAGGCTCCATATTCACCCCCGAGATGATGTGACAGCCGCCCACTGTGCTGGAAAAACT	959
OY	1053	CTTAAACATTCATGGCATTTGGAGCGGCAATTTTCCGGGATTTTGGAGAACAAATCTTTCATGTTTC	1111
Db	960	CTTAAACATTCATGGCATTTGGAGCGGCAATTTTCCGGGATTTTGGAGAACAAATCTTTCATGTTTC	1011
OY	1113	TATGAGACCGCGGATACCAAGTAAGAAAAGTATTTCTCATCCAAATTAATGACTCCAAAGCC	1173
Db	1020	TATGAGACCGCGGATACCAAGTAAGAAAAGTATTTCTCATCCAAATTAATGACTCCAAAGCC	1073
OY	1173	AAGAACATTTGACATTTGGCGCTATGAAACCTGAGAAAGCTGTGACTTTTCAACAGCCATAGTG	1233
Db	1080	AAGAACATTTGACATTTGGCGCTATGAAACCTGAGAAAGCTGTGACTTTTCAACAGCCATAGTG	1133
OY	1233	AAACCAAGTGTGTGTGCCCAACCCAGGCGATGATGTGTGACGCAGAGAACAGCTGTGCTGATTT	1293
Db	1140	AAACCAAGTGTGTGTGCCCAACCCAGGCGATGATGTGTGACGCAGAGAACAGCTGTGCTGATTT	1193
OY	1293	TCCGGGTGGGGGGCCACCGAGAGAAAAGGAAAGACCTCABAATGCTGAAACGCTGGCAAG	1353
Db	1200	TCCGGGTGGGGGGCCACCGAGAGAAAAGGAAAGACCTCABAATGCTGAAACGCTGGCAAG	1253
OY	1353	GTGCTTCTCATTTGAGACACAGATGTGCAACAGCATATGTCTATGACAAACCTGATCACA	1413
Db	1260	GTGCTTCTCATTTGAGACACAGATGTGCAACAGCATATGTCTATGACAAACCTGATCACA	1313
OY	1413	CCAGCCATGATCTGTGCCCGCTTCTGTCCAGGGGAACTGTGATTTCTTGGCAGGGGTGACAGT	1473
Db	1320	CCAGCCATGATCTGTGCCCGCTTCTGTCCAGGGGAACTGTGATTTCTTGGCAGGGGTGACAGT	1373
OY	1473	GGAGGGCCCTGTGGTCACTGTGCAAAACAAATATCTGGTGGCTGTATAGGGATTAACAACCTGG	1533
Db	1380	GGAGGGCCCTGTGGTCACTGTGCAAAACAAATATCTGGTGGCTGTATAGGGATTAACAACCTGG	1433

Oy	1533	GGTTCGTGCTCTGGCAAGCTTCACAGCCAGAGAGTGTACGGGAAATGTAGTAAATTCACG	1592
Db	1440	GGTTCGTGCTCTGCCAAAGCTTCACAGCCAGAGAGTGTACGGGAAATGTAGTAAATTCACG	1499
Oy	1593	GACTGATTTATCGACAATGAGGGCAGAGGGCTAATCCAGATGTCCTCGTCTTGACG	1652
Db	1500	GACTGATTTATCGACAATGAGGAGCAAGGGCTAATCCAGATGTCCTCGTCTTGACG	1559
Oy	1653	TCGTTTATCAAGAAACAATGGGGCTGGTTTCTGCCCTGCGATGATTACTCTAGA	1712
Db	1560	TCGTTTATCAAGAAACAATGGGGCTGGTTTCTGCCCTGCGATGATTACTCTAGA	1619
Oy	1713	GATGATTCAGAGGCTCACTTCATTTTTATTTAAACAGTGAACCTGTGCGCTTGAGCAGCT	1772
Db	1620	GATGATTCAGAGGCTCACTTCATTTTATTAACAGTGAACCTGTGCGCTTGAGCAGCT	1679
Oy	1773	CTGCCATCTTGTCGAGGCTGCACTGAGTGGCTCCCTGCGCCAGCTGCTCTCCCTAACCCCTTG	1833
Db	1680	CTGCCATCTTGTCGAGGCTGCACTGAGTGGCTCCCTGCGCCAGCTGCTCTCCCTAACCCCTTG	1733
Oy	1833	TCGCCAAGGGGTGATGAGCCGGCTGGTTGTGGGACATGGGGTCAAGTGTGA - GGAAG	1890
Db	1740	TCGCCAAGGGGTGATGAGCCGGCTGGTTGTGGGACATGGGGTCAATGTGGAAGGAAG	1799
Oy	1891	GGGTGAGAGCTG - CCCCATTGAGATCTTCTGCTGAGTCCCTTCCAGGGGCCAAATTTTG	1945
Db	1800	GGTTGGAGGCTGCCCCCATTTGAGATCTCTCTGCTGAGTCTTCCAGGGGCCAAATTTTG	1855
Oy	1950	ATGAGCATGAGAGCTGTCACTCTCACTGCTGTGATGATCTTGAGATGAAAAAGAGAGCA	2005
Db	1860	ATGAGCATGAGAGCTGTCACTCTCAGCTGTGATGATCTTGAGATGAAAAAGAGAGCA	1915
Oy	2010	TGGAAGGGAACAGCCAGAGGGCACTGAGGGGTG - CTTCTGGGGCACTTGTTAGT	2066
Db	1920	TGGAAGGGAACAGCCAGAGGGCACTGAGGGGTGCTCTGAGGGCACTTGTTAGT	1977
Oy	2059	GTCCCCAGCCTCACTCTCCACAAAGGGGATTTTCTGATGGGTCTTAGAGCCTTGAGCAGC	2128
Db	1980	GTCCCCAGCCTCACTCTCCACAAAGGGGATTTTCTGATGGGTCTTAGAGCCTTGAGCAGC	2033
Oy	2129	CCTGGATGGTGGCCAGAAATTAAGAGGACAGCCCTCATAGGGTGGTACGTGGTAGTAC	2188
Db	2037	CCTGGATGGTGGCCAGAAATTAAGAGGACAGCCCTCATAGGGTGGTACGTGGTAGTAC -	2095
Oy	2189	CTTGTAAGGGGAACAGAAATTTTCTTATATGGGGTGAAGAAATTTACAGTGGCCCT	2248
Db	2096	CTTGTAAGGGGAACAGAAATTTTCTTATATGGGGTGAAGAAATTTACAGTGGCCCT	2155
Oy	2249	GGGTGCGAGGGAAGCAATTGAAAAAGCACTTGGCCCTGAGCACTCTGTTGAGGTCTCCA	2308
Db	2156	-GGTGCAGGGGAACCAATTGAAAAAGCACTTGGCCCTGAGCACTCTGTTGAGGTCTCCA	2211
Oy	2309	CCTGCACTTGGGTGGGGGCTCTGGAGGGAAGCACTCAAGCTTCTCTCTATCTCCCTGA	2366
Db	2215	CCTGCACTTGGGTGGGGGCTCTGGAGGGAAGCACTCAAGCTTCTCTCTATCTCCCTGA	2274
Oy	2369	CCCTGCTCTAGCAACCTGTGAAGATGACATGCCCCCTTGCTCTGGCAGGGGGCCAG	2422
Db	2275	CCCTGCTCTAGCAACCTGTGAAGATG - AATGCCCTTGCTCTGGCA - GGGGCCAAG	2333
Oy	2429	TCGTGGACACATGTTGGCCTCTTACAGCCTGTAGTCACTGGAAATTGAGGTCCATGGGG	2488
Db	2332	TTTGGACACATGTGGCCTCTCTACAGCCTGTAGTCAATGGAAATTGAGGTCCATGGGG	2391
Oy	2489	AAATCAAGAGATGCTCAATTTAAGTATACATGTTTCCATGTATGTTTCTACACATTTGCT	2547
Db	2392	AAATCAAGAGATGCTCAATTTAAGTATACATGTTTCCATGTATGTTTCTACACATTTGAT	2450

RESULT 2
US-09-691-840-29
; Sequence 29, Application US/09691840
; Patent No. 6444419

GENERAL INFORMATION:
 APPLICANT: Wong, Alexander K.C.
 APPLICANT: Tavligian, Sean V.
 APPLICANT: Teng, David H.-F.
 APPLICANT: Myriad Genetics, Inc.
 TITLE OF INVENTION: TMRSS2 is a Tumor Suppressor
 FILE REFERENCE: 2318-202
 CURRENT APPLICATION NUMBER: US/09/691,840
 CURRENT FILING DATE: 2000-10-18
 PRIOR APPLICATION NUMBER: US/09/342,749
 PRIOR FILING DATE: 1999-06-29
 PRIOR APPLICATION NUMBER: US 60/091,044
 PRIOR FILING DATE: 1998-06-29
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 29
 LENGTH: 2479
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-691-840-29

Query Match 67.1%; Score 2309.4; DB 4; Length 2479;
 Best Local Similarity 98.6%; Pred. No. 0;
 Matches 2425; Conservative 0; Mismatches 21; Indels 13; Gaps 9;

QY 93 GTCATATGAAATTCAGATACCTATCATCTGATGCTGTGATMACAGCAAGATGG 152
 DB 1 GTCATATGAAATTCAGATACCTATCATCTGATGCTGTGATMACAGCAAGATGG 60
 QY 153 CTTTGAACTCAGGGTACCAACAGCTATTGGACCTTACTTGAACCAAGATGATAC 212
 DB 61 CTTTGAACTCAGGGTACCAACAGCTATTGGACCTTACTTGAACCAAGATGATAC 120
 QY 213 CGGAAACCCCTATCCGACAGCCGACGCTGGTGGCCCACTGCTACGAGGTGATCCG 272
 DB 121 CGGAAACCCCTATCCGACAGCCGACGCTGGTGGCCCACTGCTACGAGGTGATCCG 180
 QY 273 CTCAGTACTACCCGCTCCCGGAGTACGCCCCGAGGCTCTGACGACGCTTCCA 332
 DB 181 CTCAGTACTACCCGCTCCCGGAGTACGCCCCGAGGCTCTGACGACGCTTCCA 240
 QY 333 ACCCGCTGCTCTCAGCAGCAGCCCAATCCCATCCGAGAGTGTGACCTCAAGACTA 352
 DB 241 ACCCGCTGCTCTCAGCAGCAGCCCAATCCCATCCGAGAGTGTGACCTCAAGACTA 300
 QY 393 AGAAGACACTGTGATACCTGACCTGGGAGCTTCTGCTGGGAGCTGGCTGGCCG 452
 DB 301 AGAAGACACTGTGATACCTGACCTGGGAGCTTCTGCTGGGAGCTGGCTGGCCG 360
 QY 453 CTGGCTACTCTGGAATTCATGGGAGCAAGTGTCTCAACTCTGGATAGAGTGCAGT 512
 DB 361 CTGGCTACTCTGGAATTCATGGGAGCAAGTGTCTCAACTCTGGATAGAGTGCAGT 420
 QY 513 CTCAGGTAATCTCATCAACCCCTTACTGATGCTGATGGCTGTCACTGCCCCGGG 572
 DB 421 CTCAGGTAATCTCATCAACCCCTTACTGATGCTGATGGCTGTCACTGCCCCGGG 480
 QY 573 GGGAGAGCAGAAATGCTGTGTGCTGTGCTGTGAGCAAGCAACTCATCTCAGGTACT 632
 DB 481 GGGAGAGCAGAAATGCTGTGTGCTGTGCTGTGAGCAAGCAACTCATCTCAGGTACT 540
 QY 633 CATCTCAGAGAGATCTGTGACACCTGTGTGCCAAGCAGCTGGAAGCAAGTACGGG 692
 DB 541 CATCTCAGAGAGATCTGTGACACCTGTGTGCCAAGCAGCTGGAAGCAAGTACGGG 600
 QY 693 GGGGCGCTCTCAGAGAGATGGCTATAGAATATTTTACTCTAGCCAAAGAAATAGTG 752
 DB 601 GGGGCGCTCTCAGAGAGATGGCTATAGAATATTTTACTCTAGCCAAAGAAATAGTG 660
 QY 753 ATGACAGCGGATCCACAGCTTATGAATGAACCAACTGCGGCAAGTGTGATATCT 812
 DB 661 ATGACAGCGGATCCACAGCTTATGAATGAACCAACTGCGGCAAGTGTGATATCT 720

QY 813 ATAAAAAATCTATCCACAGTATGCTGTCTTCTTCAAAAGCATGGTTCTTTACGCTGA 872
 DB 721 ATAAAAAATCTATCCACAGTATGCTGTCTTCTTCAAAAGCATGGTTCTTTACGCTGT 780
 QY 873 TACCTCGGGGGTCACTTAACTCAAGCCCGCAGAGCAGATCTGGGGGAGAGCG 932
 DB 781 TACCTCGGGGGTCACTTAACTCAAGCCCGCAGAGCAGATCTGGGGGAGAGCG 840
 QY 933 CGCTCCCGGGGGCTGGCCCTGGCAGGTGACCTGACCTCCAGAACGTCACAGTGTG 992
 DB 841 CGCTCCCGGGGGCTGGCCCTGGCAGGTGACCTGACCTCCAGAACGTCACAGTGTG 899
 QY 993 GAGAGCTCATCATCACCCCGAGTGTGATGACAGCCCGCAGCTGCGTGAACAACT 1052
 DB 900 GAGAGCTCATCATCACCCCGAGTGTGATGACAGCCCGCAGCTGCGTGAACAACT 959
 QY 1053 CTTAACAATCCATGGCATTTGGAGCGGCTTTGGGGGATTTTGGAGACATCTTCAATGTC 1112
 DB 960 CTTAACAATCCATGGCATTTGGAGCGGCTTTGGGGGATTTTGGAGACATCTTCAATGTC 1019
 QY 1113 TATGAGCCCGGATACCAAGTATGAAAAAGTATTTCTATCCAAATTTATGACTCCAGAGCC 1172
 DB 1020 TATGAGCCCGGATACCAAGTATGAAAAAGTATTTCTATCCAAATTTATGACTCCAGAGCC 1079
 QY 1173 AAGAACATGATCATTTGGCTGATGAAAGCTGACAGAGCTTGAATTTCAACGACTAGTG 1232
 DB 1080 AAGAACATGATCATTTGGCTGATGAAAGCTGACAGAGCTTGAATTTCAACGACTAGTG 1139
 QY 1233 AAACCAATGTGTGCTGCCCAACCCAGAGCATATGCTGACGACCAAGACGCTGCTGAT 1292
 DB 1140 AAACCAATGTGTGCTGCCCAACCCAGAGCATATGCTGACGACCAAGACGCTGCTGAT 1199
 QY 1293 TCCGGGTGGGGGGCCACAGAGAGAAAGGAGACCTCAGAAAGTGTGAAGCGTGAACGGTCC 1352
 DB 1200 TCCGGGTGGGGGGCCACAGAGAGAAAGGAGACCTCAGAAAGTGTGAAGCGTGAACGGTCC 1259
 QY 1353 GTGCTTCTCATTTAGACACAGAGATGCAAGAGATGATGTATGACAACTGATACCA 1412
 DB 1260 GTGCTTCTCATTTAGACACAGAGATGCAAGAGATGATGTATGACAACTGATACCA 1319
 QY 1413 CCAAGCATATCTGTGCTGGCTTCTCTCAGAGGGAACGCTGATTTCCAGGGTACAGT 1472
 DB 1320 CCAAGCATATCTGTGCTGGCTTCTCTCAGAGGGAACGCTGATTTCCAGGGTACAGT 1379
 QY 1473 GGAAGGCTCTGGTCACTTGAAGAAACATATCGTGGGTGATGAGGGGATATCAAGCTGG 1532
 DB 1380 GGAAGGCTCTGGTCACTTGAAGAAACATATCGTGGGTGATGAGGGGATATCAAGCTGG 1439
 QY 1533 GGTTCCTGCTGTGCAAAAGCTTACAGACAGAGTGTACGGGAATGTGATGTATTCACG 1592
 DB 1440 GGTTCCTGCTGTGCAAAAGCTTACAGACAGAGTGTACGGGAATGTGATGTATTCACG 1499
 QY 1593 GACTGCAATTTATGACAAATGAGGCGACAGCGCTAATCCACATGTCTTCTGCTTACG 1652
 DB 1500 GACTGCAATTTATGACAAATGAGGCGCAAGCGCTAATCCACATGTCTTCTGCTTACG 1559
 QY 1653 TCGTTTACAAAGAAACAAATGAGGCGTGTGCTTCCCGCTGACATGATTTACTCTTACA 1712
 DB 1560 TCGTTTACAAAGAAACAAATGAGGCGTGTGCTTCCCGCTGACATGATTTACTCTTACA 1619
 QY 1713 GATGATTCAGAGGTCACTTCAATTTTATTTAAGAGTGAATGTCTGCTGGCTTGGCACTCT 1772
 DB 1620 GATGATTCAGAGGTCACTTCAATTTTATTTAAGAGTGAATGTCTGCTGGCTTGGCACTCT 1679
 QY 1773 CTGCAATCTGTGCAAGGCTGCAAGTGGCTCCCTGCGCAGCCTGCTCTCTTAACCCCTTG 1832
 DB 1680 CTGCAATCTGTGCAAGGCTGCAAGTGGCTCCCTGCGCAGCCTGCTCTCTTAACCCCTTG 1739
 QY 1833 TCCGCAAGGGGATATGAGCGGCTGTGAGGAGACAGTGGCGTGAAGTGTGA--GGAGAG 1890
 DB 1740 TCCGCAAGGGGATATGAGCGGCTGTGAGGAGACAGTGGCGTGAAGTGTGAAGAGAGAG 1799
 QY 1891 GGGTGAAGGCTG--CCCATGAGATCTTCTGCTGAGATCTTCTTCCAGGGGCAATTTGG 1949

Db	1800	GCCTTGGAGGGCCCCCCCATTTGAGATCTCTCTGTGAGTCTTTCACAGGGGCCAATTTTGG	1855
Qy	1950	ATGAGCATGAGAGCTGTACCTCTTCAGCTGCTGATGATCTTGAGATGAAAAGAGACACA	2009
Db	1860	ATGAGCATGAGAGCTGTACCTCTTCAGCTGCTGATGATCTTGAGATGAAAAGAGAGACA	1919
Qy	2010	TGGAAGAAGAGACAGCCAGGTGGCACCTGAGAGGGGTG-CCTGTGGGGCCATTGGTGTAGT	2068
Db	1920	TGGAAAAGGAGACAGCCAGGTGGCACCTGAGAGGGGTGCTGCTTGTGGGGCCATTGGTGTAGT	1979
Qy	2069	GTCGCCACGCTTACCTCTCCACAAGGGGATTTTGTGATGAGGGTTCTTACGCTTACAGAC	2128
Db	1980	GTCGCCACGCTTACCTTTCACAAGGGGATTTTGTGATGAGGGTTCTTACAGCCTTACGAGAC	2038
Qy	2129	CCTGGATGTGTGGCCAGAAAATTAAGAGGGACAGCCCTCATAGGGTGGAGCTGTGTGTATAC	2188
Db	2037	CCTGGATGTGTGGCCAGAAAATTAAGAGGGACAGCCCTCATAGGGTGGAGCTGTGTGTATAC	2095
Qy	2189	CTTGTAAAGGGGAAACAGAAACATTTTGTCTTAATGGGGTGAGAAATATAGACAGTACCCCTT	2248
Db	2096	CTTGTAAAGGGGAAACAGAAACATTTTGTCTTAATGGGGTGAGAAATATAGACAGTACCCCTT	2155
Qy	2249	GGGGTCCAGAGGAAAGCAATTTGAAAAGAACATGTGCCCTGACACTCTCTGTGTATCTCTCCCA	2308
Db	2156	-GGTCCAGAGGAAAGCAATTTGAAAAGAACATGTGCCCTGACACTCTCTGTGTATCTCTCCCA	2214
Qy	2309	CCTGCACATTGGGTGGGGCTCTGGGAGGGAGACTAGGCTTCTCTCTATCTCTCCCTGA	2368
Db	2215	CCTGCACATTGGGTGGGGCTCTGGGAGGGAGACTAGGCTTCTCTCTATCTCTCCCTGA	2274
Qy	2369	CCCTGTCTTCAGACCTCTGAGAGTGCACATGCCCCCTTGTGTCTGTGGCAGGGGGCCCAAG	2428
Db	2275	CCCTGTCTTCAGACCTCTGAGAGTGCACATGCCCCCTTGTGTCTGTGGCAGGGGGCCCAAG	2331
Qy	2429	TCTGTGCACATGTGGGCTCTTTCAGGCTGTGCTAGTCACTGGAATAATGAGAGTTCATAGGGGG	2488
Db	2332	TTTGTGCACATGTGGGCTCTTTCAGGCTGTGATGTCATTGGAATAATGAGAGTTCATAGGGGG	2391
Qy	2489	AAATCAAGATGCTCAATTTTAAGGTATACATGCTGTTCCATGTATATGTTTCTACACATTTGCT	2547
Db	2392	AAATCAAGATGCTCAATTTTAAGGTATACATGCTGTTCCATGTATATGTTTCTACACATTTGAT	2450

RESULT 3
US-09-342-749-1
; Sequence 1, Application US/09342749

```

GENERAL INFORMATION:
APPLICANT: Wong, Alexander K.C.
APPLICANT: Tavtiglian, Sean V.
APPLICANT: Teng, David H.-F.
APPLICANT: Myriad Genetics, Inc.
TITLE OF INVENTION: TMPRSS2 Is a Tumor Suppressor
FILE REFERENCE: 2318-202
CURRENT APPLICATION NUMBER: US/09/342,749
CURRENT FILING DATE: 1999-06-29
EARLIER APPLICATION NUMBER: US 60/091,044
EARLIER FILING DATE: 1998-06-29
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1479
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1476)
FEATURE:
NAME/KEY: conflict
LOCATION: (724)
OTHER INFORMATION: Listed as T in GenBank Accession NO. D753325
FEATURE:

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1 NAME/KEY: conflict
2 LOCATION: (985)
3 OTHER INFORMATION: Listed as C in GenBank Accession No. 6166194 U75329
4 FEATURE:
5 NAME/KEY: conflict
6 LOCATION: (1347)
7 OTHER INFORMATION: Listed as C in GenBank Accession No. 6166194 U75329
8 FEATURE:
9 NAME/KEY: conflict
10 LOCATION: (1466)
11 OTHER INFORMATION: Listed as A in GenBank Accession No. 6166194 U75329
12 FEATURE:
13 NAME/KEY: conflict
14 LOCATION: (1471)
15 OTHER INFORMATION: Listed as A in GenBank Accession No. 6166194 U75329.
16 FEATURE:
17 NAME/KEY: allele
18 LOCATION: (478)
19 OTHER INFORMATION: This base can be G or A with G being the more
20 OTHER INFORMATION: common allele. The codon will change from Val to
21 OTHER INFORMATION: Met.
22 FEATURE:
23 NAME/KEY: allele
24 LOCATION: (777)
25 OTHER INFORMATION: This base can be C or T with C being the more
26 OTHER INFORMATION: common allele. The codon is unaffected with both
27 OTHER INFORMATION: alleles encoding Gly.
28 FEATURE:
29 NAME/KEY: allele
30 LOCATION: (768)
31 OTHER INFORMATION: This base can be C or T with C being the more
32 OTHER INFORMATION: common allele. This is a silent polymorphism.
33 FEATURE:
34 NAME/KEY: allele
35 LOCATION: (834)
36 OTHER INFORMATION: This base can be C or T with C being the more
37 OTHER INFORMATION: common allele. This is a silent polymorphism.
38 FEATURE:
39 NAME/KEY: allele
40 LOCATION: (625)
41 OTHER INFORMATION: This base can be T or A with T being the more
42 OTHER INFORMATION: common allele. The codon will change from Phe to
43 OTHER INFORMATION: Ile
44 US-09-342-749-1

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Query Match	42.68; Score 1468; DB 4; Length 1479;
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Matches 1479; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 149 ATGGCTTGAACCTCAGGGTCACCACCAGCTATTGGACCTTACTATGAAAAACCATGGATAC 208

db : 1 ATGCTTGAACCTCAGGCTCACCACGCTATTGGACCTACTATGAAAACCATGATAC 60

09 209 CAAACGGAACAATCCAGCCACCTGGTCCCACTGGTCACAGCCTCCAT 268

61 |||||

QUESTION

[illegible]

DD 121 CCBGCICAGIACCCCGICCCCCGIAGCAGIACGCCCCGAGGICCIAGAGCAGGCT 180

329 TCCAACCCCGTCCGTCGACGCGCCCAATCCCCATCCGGACAGTGTGCACCTCAAG 388

Db 181 TCCAACCCCGTCTGACAGCAGCCAAATCCCCTCCGGACAGTGTGCACCTCAAG 240

389 ACTAAGAGCACTGTGCATCACCTTGACCCCTGGGACCTTCCTCGTGGAGCTGCGCTG 448

Db 241 ACTAAGAAGCACTGTGCATCACCTTGACCCCTGGGACCTTCCTCGTGGAGCTGCGCTG 300

QY 449 GCCGCTGGCTACTCTGGAAGTTCATGGGCAGCAAGTGTCTCCAAGTGGGATAGAGTGC 508

Db 301 GCCGCTGGCTACTCTGGAGTTCATGGGCAGCAAGTCTCCAACTCTGGATAGAGTGC 360

[illegible]

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DB      1440 CACGCACTGGATTTCACCAATAGCGCAGACGGCTAA 1479
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RESULT 4
US-09-691-840-1
; Sequence 1, Application US/09691840
; Patent No. 6444419
; GENERAL INFORMATION:
; APPLICANT: Wong, Alexander K.C.
; APPLICANT: Tavligian, Sean V.
; APPLICANT: Teng, David H.-F.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: TPMSR2 is a Tumor Suppressor
; FILE REFERENCE: 2318-202
; CURRENT APPLICATION NUMBER: US/09/691,840
; CURRENT FILING DATE: 2000-10-18
; PRIOR APPLICATION NUMBER: US/09/342,749
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 60/091,044
; PRIOR FILING DATE: 1998-06-29
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1476)
; NAME/KEY: conflict
; LOCATION: (724)
; OTHER INFORMATION: Listed as T in GenBank Accession NO. U75329
; NAME/KEY: conflict
; LOCATION: (985)
; OTHER INFORMATION: Listed as C in GenBank Accession No. 6444419 U75329
; NAME/KEY: conflict
; LOCATION: (1347)
; OTHER INFORMATION: Listed as C in GenBank Accession No. 6444419 U75329
; NAME/KEY: conflict
; LOCATION: (1466)
; OTHER INFORMATION: Listed as A in GenBank Accession No. 6444419 U75329
; NAME/KEY: conflict
; LOCATION: (1471)
; OTHER INFORMATION: Listed as A in GenBank Accession No. 6444419 U75329.
; NAME/KEY: allele
; LOCATION: (4478)
; OTHER INFORMATION: This base can be G or A with G being the more
; OTHER INFORMATION: common allele. The codon will change from Val to
; OTHER INFORMATION: Met.
; NAME/KEY: allele
; LOCATION: (777)
; OTHER INFORMATION: This base can be C or T with C being the more
; OTHER INFORMATION: common allele. The codon is unaffected with both
; OTHER INFORMATION: alleles encoding Gly.
; NAME/KEY: allele
; LOCATION: (768)
; OTHER INFORMATION: This base can be C or T with C being the more
; OTHER INFORMATION: common allele. This is a silent polymorphism.
; NAME/KEY: allele
; LOCATION: (834)
; OTHER INFORMATION: This base can be C or T with C being the more
; OTHER INFORMATION: common allele. This is a silent polymorphism.
; NAME/KEY: allele
; LOCATION: (625)
; OTHER INFORMATION: This base can be T or A with T being the more
; OTHER INFORMATION: common allele. The codon will change from Phe to Ile
US-09-691-840-1
Query Match          42.6%; Score 1468; DB 4; Length 1479;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1479; Conservative 0; Mismatches 0; Indels 1; Gaps 1.
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QY 149 ATGGCTTTGAATCAAGGCTCACCACAGCTATTGGACCTTACTATGAAACCATGATAC 208
|||||
Db 1 ATGGCTTTGAATCAAGGCTCACCACAGCTATTGGACCTTACTATGAAACCATGATAC 60
QY 209 CAACCGGAAACCCCTATCCCGCACAGCCAGCTGTGTCCCGACGTCTACGAGGTCAT 268
|||||
Db 61 CAACCGGAAACCCCTATCCCGCACAGCCAGCTGTGTCCCGACGTCTACGAGGTCAT 120
QY 269 CCGGCTCACTACTACCCGTCGCCCGTACGAGTACGCCCGAGGATCCGACGAGCT 328
121 CCGGCTCACTACTACCCGTCGCCCGTACGAGTACGCCCGAGGATCCGACGAGCT 180
QY 329 TCCAAACCCGCTGTGTGACGACGACCCAAATCCCAATCCGAGACAGTGTGCACTCAAG 388
Db 181 TCCAAACCCGCTGTGTGACGACGACCCAAATCCCAATCCGAGACAGTGTGCACTCAAG 240
QY 389 ACTAAGAAAGCACTGTGATCACTTGAACCTTGGGAGACCTTCTGAGGATGCGCTG 448
Db 241 ACTAAGAAAGCACTGTGATCACTTGAACCTTGGGAGACCTTCTGAGGATGCGCTG 300
QY 449 GCGGCTGCGCTACTGTGAAAGTTCATGGGACAGCAAGTGTCCAACTCTGGATAGAGTC 508
301 GCGGCTGCGCTACTGTGAAAGTTCATGGGACAGCAAGTGTCCAACTCTGGATAGAGTC 360
QY 509 GACTCTCAAGTACTGTGATCAACCCCTTAACCTGTGTGATGGCGTGTCAACACTGCCCC 568
Db 361 GACTCTCAAGTACTGTGATCAACCCCTTAACCTGTGTGATGGCGTGTCAACACTGCCCC 420
QY 569 GCGGAGGAGAGCAAGATGGTGTGTGCTGTACGAGCAAACTCTCATCTTCAGGTG 628
Db 421 GCGGAGGAGAGCAAGATGGTGTGTGCTGTACGAGCAAACTCTCATCTTCAGGTG 480
QY 629 TACTCATCTCAGAGAAAGTCTGTGGACCCCTGTGTGCAAGACAGTGTGAAACAGATAC 688
Db 481 TACTCATCTCAGAGAAAGTCTGTGGACCCCTGTGTGCAAGACAGTGTGAAACAGATAC 540
QY 689 GGGCGGGCGGCTGTGAGGACATGGGCTATGAAGATATTTTACTCTACCAAGAAAT 748
Db 541 GGGCGGGCGGCTGTGAGGACATGGGCTATGAAGATATTTTACTCTACCAAGAAAT 600
QY 749 GTGGATGACAGGAGATCCACGAGCTTTATGAACATGAACAGAGTCCGGCAATGCGAT 808
Db 601 GTGGATGACAGGAGATCCACGAGCTTTATGAACATGAACAGAGTCCGGCAATGCGAT 660
QY 809 ATCTATAAAAAACTGTACCAAGATGATGCTTCTTCAAAAGCAGTGTCTTTTACGC 868
Db 661 ATCTATAAAAAACTGTACCAAGATGATGCTTCTTCAAAAGCAGTGTCTTTTACGC 720
QY 869 TGTATAGCTGTGGGGGTCACTTGAATCTAACCCCGCAGAGCAGATGCTGGCGGAG 928
Db 721 TGTATAGCTGTGGGGGTCACTTGAATCTAACCCCGCAGAGCAGATGCTGGCGGAG 780
QY 929 ACCGGGCTCCGGGGGCTGGGCGAGGTCAAGCTGCAAGTCCAGATGCTCAGCT 988
Db 781 ACCGGGCTCCGGGGGCTGGGCGCT- GGCAGGTCAAGCTGCAAGTCCAGATGCTCAGCT 839
QY 989 GTGCGAGGCTCCATCATCACCCCGAGTGTGATGTCGACAGCCGCACTGCTGGAAAA 1048
Db 840 GTGCGAGGCTCCATCATCACCCCGAGTGTGATGTCGACAGCCGCACTGCTGGAAAA 899
QY 1049 ACCCTTAAACATTCATGGCATTTGACGAGCATTTGGGGGATTTTGAGCAATCTTTTCA 1108
Db 900 ACCCTTAAACATTCATGGCATTTGACGAGCATTTGGGGGATTTTGAGCAATCTTTTCA 959
QY 1109 GTTCTATGAGCGGATACCAAGTAGAAAAAGTAGTTTCTCATCAAAATATAGCTCCAA 1168
Db 960 GTTCTATGAGCGGATACCAAGTAGAAAAAGTAGTTTCTCATCAAAATATAGCTCCAA 1019
QY 1169 GACCAAGAACATGACATTTGCGCTGTGAGAGCTGCAAGAGCTTGTACCTTACAGACT 1228
Db 1020 GACCAAGAACATGACATTTGCGCTGTGAGAGCTGCAAGAGCTTGTACCTTACAGACT 1079
QY 1229 AGTGAACACAGTGTGTGTGCGCAACCCAGCATGATGCTGCAAGCAAGAACCTGTGCTG 1288

Db 1080 AGTGAACACAGTGTGTGTGCGCAACCCAGCATGATGCTGCAAGCAAGAACCTGTGCTG 1139
QY 1289 GATTTCCGGGTGGGGGCGCACCGAGAGAGAAAGAACCTCAGAAAGTGTGAACGCTGC 1348
Db 1140 GATTTCCGGGTGGGGGCGCACCGAGAGAGAAAGAACCTCAGAAAGTGTGAACGCTGC 1199
QY 1349 CAAGTGTCTTCATTTGACACAGAGATGCAACAGCAGATATGCTATGACAACTGAT 1408
Db 1200 CAAGTGTCTTCATTTGACACAGAGATGCAACAGCAGATATGCTATGACAACTGAT 1259
QY 1409 CACACAGCATGATCTGTGCGGCTTCTGTCAGGGGAACTGCAATTTCTTCCAGGCTGA 1468
Db 1260 CACACAGCATGATCTGTGCGGCTTCTGTCAGGGGAACTGCAATTTCTTCCAGGCTGA 1319
QY 1469 CAGTGAGGCGCTGTGCTACTTGCAGAAACATATCTGTGTGATAGGGGATACAAAG 1528
Db 1320 CAGTGAGGCGCTGTGCTACTTGCAGAAACATATCTGTGTGATAGGGGATACAAAG 1379
QY 1529 CTGGGGTCTGTGCTGTGCCAAAGCTTACAGACAGAGAGTGTACGGGAATGTGATGAT 1588
Db 1380 CTGGGGTCTGTGCTGTGCCAAAGCTTACAGACAGAGAGTGTACGGGAATGTGATGAT 1439
QY 1589 CACGAGCTGATTTATCGACAAATGAGGCGACAGCGCTAA 1628
Db 1440 CACGAGCTGATTTATCGACAAATGAGGCGACAGCGCTAA 1479

RESULT 5
US-08-807-151-2
; Sequence 2, Application US/08807151
; Patent No. 6043033
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; TITLE OF INVENTION: NOVEL HUMAN PROSTATE-ASSOCIATED
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/807,151
; FILING DATE: Filed Herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0227 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1077 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SCORNIOT01
; CLONE: 556016

US-08-807-151-2

Query Match	28.6%;	Score 983;	DB 3;	Length 1077;
Best Local Similarity	-99.8%;	Pred. No. 3.2e-256;		
Matches 994; Conservative	0;	Mismatches 1;	Indels 1;	Gaps 1

QY	758	AGCGATATCCACAGCTTTATGAAATCGAACAAGATGCCGGCAATGCAATATCAATAAA	817
Db	83	AGCGGATATCCACAGCTTTATGAAATCTGACACAGATGCCGGCAATGCAATATCAATAAA	142
QY	818	AAACTGTACCAAGTGTATGCCGTCTTCAAAAGCAGTGGTTCTTACGTGTATAGCC	877
Db	143	AAACTGTACCAAGTGTATGCCGTCTTCAAAAGCAGTGGTTCTTACGTGTATAGCC	202
QY	878	TGCGGGGTCAACTTGAACCTAAGCCGCGACAGCAGATGCTGGGGGGGAGAGCGCGCTC	937
Db	203	TGCGGGGTCAACTTGAACCTAAGCCGCGACAGCAGATGCTGGGGGGGAGAGCGCGCTC	262
QY	938	CCGGGGGGCGTGGGGCGAGGTGCAGCGCTGCAGAAAGCTCCAGCTGTGGGGGAGG	997
Db	263	CCGGGGGGCGTGGGGCGAGGTGCAGCGCTGCAGAAAGCTCCAGCTGTGGGGGAGG	321
QY	998	CTCCATCATCACCCCGCAGTGGATCTGTGACAGCCGCCACCTGCGTGGAAAAACCTTTAA	1057
Db	322	CTCCATCATCACCCCGCAGTGGATCTGTGACAGCCGCCACCTGCGTGGAAAAACCTTTAA	381
QY	1058	CAATCCATGCGATTGGACGGCATTTCGGGGGATTTTGAACAATCTTTCATGTTCTATGG	1117
Db	382	CAATCCATGCGATTGGACGGCATTTCGGGGGATTTTGAACAATCTTTCATGTTCTATGG	441
QY	1118	AGCCGATACCAAGTATGAAAAAGTGATTTCTCATCCAAATTTATGATCCCAAGCCAAAGA	1177
Db	442	AGCCGATATCCAAAGTATGAAAAAGTGATTTCTCATCCAAATTTATGACTCCAAAGCCAAAGA	501
QY	1178	CAATGACATTGGCGCTGATGAGGTGCGAAGCCCTGTGACTTTCCAAAGCAGCTAGTGAACC	1237
Db	502	CAATGACATTGGCGCTGATGAGGTGCGAAGCCCTGTGACTTTCCAAAGCAGCTAGTGAACC	561
QY	1238	AGTGTGCTGCTGCCAACCCAGGCAATGATCTGCGACCCAGAAACAGCTTGTGGATTTCCGG	1297
Db	562	AGTGTGCTGCTGCCAACCCAGGCAATGATCTGCGACCCAGAAACAGCTTGTGGATTTCCGG	621
QY	1298	GTCGGGGGGCCACGAGAGGAAAAAGGAGAACCTTAGAAGTCTGCAAGCGTGCACAAAGTGCT	1357
Db	622	GTCGGGGGGCCACGAGAGGAAAAAGGAGAACCTTAGAAGTCTGCAAGCGTGCACAAAGTGCT	681
QY	1358	TCTCATTTGAGACACAGAGATGCAACAGCAGATATGTCTATGACAACTGATACACACAC	1417
Db	682	TCTCATTTGAGACACAGAGATGCAACAGCAGATATGTCTATGACAACTGATACACACAC	741
QY	1418	CATCATCTGTGCGCGCTTCTCTGCAAGGGAAAGCTGCATTTCTTGCACAGGTGCACAGTGGAGG	1477
Db	742	CATCATCTGTGCGCGCTTCTCTGCAAGGGAAAGCTGCATTTCTTGCACAGGTGCACAGTGGAGG	801
QY	1478	GCCCTGTGCTACTTTCGAAGAAACAATATCTGTTGGTGTGATAGGGGATACAAGCTGGGGTTTC	1537
Db	802	GCCCTGTGCTACTTTCGAAGAAACAATATCTGTTGGTGTGATAGGGGATACAAGCTGGGGTTTC	861
QY	1538	TGCGCTGTCCAAAGCTTACAGACCCAGGAGTGTACGGGAAATGTGATGTTTACACGAGACTG	1597
Db	862	TGCGCTGTCCAAAGCTTACAGACCCAGGAGTGTACGGGAAATGTGATGTTTACACGAGACTG	921
QY	1598	GATTATTCGACAAATGAGGGCAGACGGCTTAATCCACATGCTGTGCTCTTACACGCTGCT	1657
Db	922	GATTATTCGACAAATGAGGGCAGACGGCTTAATCCACATGCTGTGCTCTTACACGCTGCT	981
QY	1658	TTACAAAGAAACAATGGGGCTGTTTTGCTTCCCGCTGATGATGATTTACTCTTAGAGATGA	1717
Db	982	TTACAAAGAAACAATGGGGCTGTTTTGCTTCCCGCTGATGATGATTTACTCTTAGAGATGA	1041
QY	1718	TTTCAGAGTCACTTCAATTTTATTTAAACAGTGAAC	1753
Db	1042	TTTCAGAGTCACTTCAATTTTATTTAAACAGTGAAC	1077

RESULT 6
US-09-478-957-2
; Sequence 2, Application US/09478957

```

1  GENERAL INFORMATION:
2  APPLICANT: Bandman, Olga
3  APPLICANT: Lal, Preeti
4  TITLE OF INVENTION: NOVEL HUMAN PROSTATE-ASSOCIATED
5  TITLE OF INVENTION: PROTEASE
6  NUMBER OF SEQUENCES: 5
7  CORRESPONDENCE ADDRESS:
8  ADDRESSEE: Incyte Pharmaceuticals, Inc.
9  STREET: 3174 Potler Drive
10 CITY: Palo Alto
11 STATE: CA
12 COUNTRY: US
13 ZIP: 94304
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Diskette
16 COMPUTER: IBM Compatible
17 OPERATING SYSTEM: DOS
18 SOFTWARE: FASTSEQ Version 2.0
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/09/478,957
21 FILING DATE:
22 CLASSIFICATION:
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: 08/807,151
25 FILING DATE:
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Billings, Lucy J.
28 REGISTRATION NUMBER: 36,749
29 REFERENCE/DOCKET NUMBER: PF-0227 US
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: 415-845-0555
32 TELEFAX: 415-845-4166
33 INFORMATION FOR SEQ ID NO: 2:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 1077 base pairs
36 TYPE: nucleic acid
37 STRANDEDNESS: single
38 TOPOLOGY: linear
39 IMMEDIATE SOURCE:
40 LIBRARY: SCORNO701
41 CLONE: 556016
42
43 US-09-478-957-2

```

Query Match	28.6%	Score 983;	DB 4;	Length 1077;
Best Local Similarity	99.8%	Pred. No. 3.2e-256;		
Matches 994;	Conservative	0;	Mismatches 1;	Indels 1;
				Gaps 1;

QY	758	AGGGATATCAACACACTTTATGAAACATGAAACACAAAGTGGCGCAATGCGATATCTTAA	817
Db	83	AGCGGATTCACACACACTTTATGAACTGTAACAAAGTGGCGCAATGCGATATCTTAA	142
QY	818	AAACTGTACCACTGATGCGCTGTTCTTCAAAAGCAGTGGTTCCTTACGCTGTATAGCC	877
Db	143	AAACTGTACCACTGATGCGCTGTTCTTCAAAAGCAGTGGTTCCTTACGCTGTATAGCC	202
QY	878	TGGGGGGCAACTTGAGCTCAAGCGCGCAAGAGATCTGGGGCGGAGACGGCGTTC	937
Db	203	TGGGGGGCAACTTGAGCTCAAGCGCGCAAGAGATCTGGGGCGGAGACGGCGTTC	262
QY	938	CCGGGGGCGTTGGCCCTTGGGCGAGGTCACTGCACGTCACAAAGTCCACGTTGGCGAAG	997
Db	263	CCGGGGGCGTTGGCCCTTGGGCGAGGTCACTGCACGTCACAAAGTCCACGTTGGCGAAG	321
QY	998	CTTCATATACCCCGAAGTGGATCGTGAACGCCGCCACTGCGTGTAAGAAAACCTTTAA	1057
Db	322	CTTCATATACCCCGAAGTGGATCGTGAACGCCGCCACTGCGTGTAAGAAAACCTTTAA	381

QY 1058 CAATTCATGGAATGAGACGGCATTTCCGGGAAATTTGAGACAAATCTTTCATCTTCTAAGG 1117
Db 382 CAATTCATGGAATGAGACGGCATTTCCGGGAAATTTGAGACAAATCTTTCATCTTCTAAGG 441
QY 1118 AGCCGATACCAAGTAGAAAAAGTGAATTTCTCATTCCAAATTTATGACTCCAAAGACCAAGAA 1177
Db 442 AGCCGATACCAAGTAGAAAAAGTGAATTTCTCATTCCAAATTTATGACTCCAAAGACCAAGAA 501
QY 1178 CAATGACATTTGCGGTGATGAAAGCTGCAGAAAGCTCTGACTTTTCAACGACCTTAGTAAMAC 1237
Db 502 CAATGACATTTGCGGTGATGAAAGCTGCAGAAAGCTCTGACTTTTCAACGACCTTAGTAAMAC 561
QY 1238 AGTGTGCTGCGCCCAACCCAGGACATGATGCTGCAGACCAAGACAGCTCTGCTGGATTTCCGG 1297
Db 562 AGTGTGCTGCGCCCAACCCAGGACATGATGCTGCAGACCAAGACAGCTCTGCTGGATTTCCGG 621
QY 1298 GTGGGGGGGCCACGAGGAGAAAGGGAAGACCTCAGAAGTGTCTGAACGCTGCGCCAAAGTGCT 1357
Db 622 GTGGGGGGGCCACGAGGAGAAAGGGAAGACCTCAGAAGTGTCTGAACGCTGCGCCAAAGTGCT 681
QY 1358 TCTCATTTGAGACACAGAGATGCAACAGCAGATATGTCTATGACAAACCTGATCACACAGC 1417
Db 682 TCTCATTTGAGACACAGAGATGCAACAGCAGATATGTCTATGACAAACCTGATCACACAGC 741
QY 1418 CATGATCTGTCGCGCGCTTCTCTGAGGGGAAGCGCATTTCTTCCAGGGGTGACAGTGGAGG 1477
Db 742 CATGATCTGTCGCGCGCTTCTCTGAGGGGAAGCGCATTTCTTCCAGGGGTGACAGTGGAGG 801
QY 1478 GCGTCTGCTACTTTCGAAAGCAATATCTGTGGTCTGATGAGGGGATACAAAGCTGGGGTTC 1537
Db 802 GCGTCTGCTACTTTCGAAAGCAATATCTGTGGTCTGATGAGGGGATACAAAGCTGGGGTTC 861
QY 1538 TGCGTGTGCCAAAGCTTACAGACCAGAGTGTACGGGAATGTGATGTATTCACGAGCTG 1597
Db 862 TGCGTGTGCCAAAGCTTACAGACCAGAGTGTACGGGAATGTGATGTATTCACGAGCTG 921
QY 1598 GATTATTCGCAAAATGAGGGCAGACGGCTATTCACATAGTGTCTGCTCTGACGCTGT 1657
Db 922 GATTATTCGCAAAATGAGGGCAGACGGCTATTCACATAGTGTCTGCTCTGACGCTGT 981
QY 1658 TTACAGAAAAAATGAGGGCGCTGTTTGGCTTCCCGTGCATGATTACTCTTAGAGATGA 1717
Db 982 TTACAGAAAAAATGAGGGCGCTGTTTGGCTTCCCGTGCATGATTACTCTTAGAGATGA 1041
QY 1718 TTACAGAGTCATCTCATTTTATTTAAACAGTGAAT 1753
Db 1042 TTACAGAGTCATCTCATTTTATTTAAACAGTGAAT 1077

RESULT 7
US-09-605-785-384
Sequence 384, Application US-09-605785
Patent No. 6321716.
GENERAL INFORMATION:
APPLICANT: Xu, Jifengchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvyck, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

7
W. von Rosenberg

```

1 FILE REFERENCE: 210121.427C16
2 CURRENT APPLICATION NUMBER: US-09/605,785
3 CURRENT FILING DATE: 2000-06-27
4 NUMBER OF SEQ ID NOS: 835
5 SOFTWARE: FASTSEQ for Windows Version 3.0
6 SEQ ID NO 384
7 LENGTH: 557
8 TYPE: DNA
9 ORGANISM: Homo sapiens
10 US-09-605-785-384
11
12 Query Match          14.2%: Score 490; DB 4; Length 557;
13 Best Local Similarity 98.0%; Pred. No. 6,2e-123;
14 Matches 496; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
15
16 QY 2717 AAAGTCCCATGTCGTGGCGGCAGAAAGAAGATGTCTTTTGTTTGGACTCTCTGTGG 2776
17      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
18 Db 32 AAAATGCCGGCGCGCTGCACGAGAAAGAAAGATGTCTTTTGTTTGGACTCTCTGTGG 91
19
20 QY 2777 TCCCTTCCAATGCTGTGGGTTTCCCAACGAGGGAAGGTCCTTTTGCAATTGCCAAGTGC 2836
21      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
22 Db 92 TCCTCTTCCAAGTCTGTGGGTTTCCCAACGAGGGAAGGTCCTTTTGCAATTGCCAAGTGC 151
23
24 QY 2837 CATACCAATGAGCATCTACTCTACATACATGCTGCTCCCTGGCCAGACAGGCTGTTTGA 2896
25      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
26 Db 152 CATACCAATGAGCATCTACTCTACATACATGCTGCTCCCTGGCCAGACAGGCTGTTTGA 211
27
28 QY 2897 AGAATGAATGAATGAATGATTTCTACAGCTTAGACATTAACCTTGAATAAGAAAGTCTTCCAATC 2956
29      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
30 Db 212 AGAATGAATGAATGAATGATTTCTACAGCTTAGACATTAACCTTGAATAAGAAAGTCTTCCAATC 271
31
32 QY 2957 CCATTTCGACAGATCCGCTGTGTGCACATGCTCTGTAGAGAGACGACATTCGCCAGGACCTT 3016
33      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 Db 272 CCATTTCGACAGATCCGCTGTGTGCACATGCTCTGTAGAGAGACGACATTCGCCAGGACCTT 331
35
36 QY 3017 GGAAACCACTTGGACATGTAAAGTGCTGTGCTCCCAAGACACATCCTTAAGAGGTGTGTAA 3076
37      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
38 Db 332 GGAAACCACTTGGACATGTAAAGTGCTGTGCTCCCAAGACACATCCTTAAGAGGTGTGTAA 391
39
40 QY 3077 TGCTGAAAACGCTCTCTCTTTTATTTGCCCCCTCTTATTTATGTGAACAACGTGTGTCT 3136
41      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
42 Db 392 TGCTGAAAACGCTCTCTCTTTTATTTGCCCCCTCTTATTTATGTGAACAACGTGTGTCT 451
43
44 QY 3137 TTTTTTGTATCTTTTAACTGAAGTGAAGTCAATGTGAATAATGAATATCATGCAAATAA 3196
45      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
46 Db 452 TTTTTTGTATCTTTTAACTGAAGTGAAGTCAATGTGAATAATGAATATCATGCAAATAA 511
47
48 QY 3197 ATTATGCAATTTTTTTTCCAAAGTAA 3222
49      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
50 Db 512 ATTATGCAATTTTTTTTCCAAAGTAA 537
51
52 RESULT 8
53 US-09-439-313-384
54 Sequence 384, Application US/09439313
55 Patent No. 6329505
56 GENERAL INFORMATION:
57 APPLICANT: Xu, Jiangchun
58 APPLICANT: Dillon, Davin C.
59 APPLICANT: Mitchem, Jennifer L.
60 APPLICANT: Harlocker, Susan Louise
61 APPLICANT: Jjiang Yuqul
62 APPLICANT: Reed, Steven G.
63 APPLICANT: Kalos, Michael
64 APPLICANT: Fanger, Gary
65 APPLICANT: Retter, Mark
66 APPLICANT: Solk, John
67 APPLICANT: Day, Craig
68 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
69 FILE REFERENCE: 210121.427C9
70 CURRENT APPLICATION NUMBER: US/09/439,313
71 CURRENT FILING DATE: 1999-11-12

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Db 301 GTCCTTTTGCATGTCAGATGCCATACCATGACGACTACGCTACCATGCTTTCGCTC 360
Qy 2874 CTGGCCACAGCAGCTGCTTTCAGAGATGAATGAATGAT 2913
Db 361 CTGGCCACAGCAGCTGCTTTCAGAGATGAATGAATGAT 400

RESULT 13
US-09-232-149A-325
; Sequence 325, Application US/09232149A
; Patent No. 6465611
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
; FILE REFERENCE: 210121.427C6
; CURRENT APPLICATION NUMBER: US/09/232,149A
; CURRENT FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 338
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 325
; LENGTH: 400
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-232-149A-325

Query Match 11.6%; Score 398.4; DB 4; Length 400;
Best Local Similarity 99.8%; Pred. No. 3.2e-98;
Matches 399; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2514 ACAGTGTTCACATGTTATGTTCTTACACATGCTACCTGAGTCTCTGGAACCTAGCT 2573
Db 1 ACAGTGTTCACATGTTATGTTCTTACACATGCTACCTGAGTCTCTGGAACCTAGCT 60
Qy 2574 TTTGATGTCTCCAGATGACGACCTTCATTTAACTCTTTGAACCTGATCATCTTTGCCA 2633
Db 61 TTTGATGTCTCCAGATGACGACCTTCATTTAACTCTTTGAACCTGATCATCTTTGCCA 120
Qy 2634 AGTAAGAGTGTGGCTTATTTGAGTGTGCTTTCACAAATGACTGGCTCCGACTTAAGCT 2693
Db 121 AGTAAGAGTGTGGCTTATTTGAGTGTGCTTTCACAAATGACTGGCTCCGACTTAAGCT 180
Qy 2694 TCTATAAATGAATGTGCTGAGCAAGTCCCATGCTGAGGCGGGAAGAGAAAGATGT 2753
Db 181 TCTATAAATGAATGTGCTGAGCAAGTCCCATGCTGAGGCGGGAAGAGAAAGATGT 240
Qy 2754 GTTTTGTGAGCTCTCTGTGTGCTCCCTTCGCAATGCTGTGGGTTTCCAAACAGGGGAAG 2813
Db 241 GTTTTGTGAGCTCTCTGTGTGCTCCCTTCGCAATGCTGTGGGTTTCCAAACAGGGGAAG 300
Qy 2814 GTCCTTTTGCATGTCAGATGCCATACCATGACGACTACCTACCATGCTTTCGCTC 2873
Db 301 GTCCTTTTGCATGTCAGATGCCATACCATGACGACTACCTACCATGCTTTCGCTC 360
Qy 2874 CTGGCCACAGCAGCTGCTTTCAGAGATGAATGAATGAT 2913
Db 361 CTGGCCACAGCAGCTGCTTTCAGAGATGAATGAATGAT 400

RESULT 14
US-09-605-785-401
; Sequence 401, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqi
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
```

```
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Wang, Aijun
; APPLICANT: Skelky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C16
; CURRENT APPLICATION NUMBER: US/09/605,785
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 401
; LENGTH: 355
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(355)
; OTHER INFORMATION: n = A,T,C or G
US-09-605-785-401
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Query Match 10.2%; Score 352; DB 4; Length 355;
Best Local Similarity 99.2%; Pred. No. 1.1e-85;
Matches 352; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2516 ACAGTGTTCACATGTTATGTTCTTACACATGCTACCTGAGTCTCTGGAACCTAGCTT 2575
Db 1 ACAGTGTTCACATGTTATGTTCTTACACATGCTACCTGAGTCTCTGGAACCTAGCTT 60
Qy 2576 TGATGTCTCCAGATGACGACCTTCATTTAACTCTTTGAACCTGATCATCTTTGCCA 2635
Db 61 TGATGTCTCCAGATGACGACCTTCATTTAACTCTTTGAACCTGATCATCTTTGCCA 120
Qy 2636 TAAGAGTGTGGCTTATTTGAGTGTGCTTTCACAAATGACTGGCTCCGACTTAAGCT 2695
Db 121 TAAGAGTGTGGCTTATTTGAGTGTGCTTTCACAAATGACTGGCTCCGACTTAAGCT 180
Qy 2696 TATATAATGAATGTGCTGAGCAAGTCCCATGCTGAGGCGGGAAGAGAAAGATGT 2755
Db 181 TATATAATGAATGTGCTGAGCAAGTCCCATGCTGAGGCGGGAAGAGAAAGATGT 240
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Qy 2816 CCGTTTGCATGTCAGATGCCATACCATGACGACTACCTACCATGCTTTCGCTC 2870
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RESULT 15
US-09-439-313-401
; Sequence 401, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Marc
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
```

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; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 401
; LENGTH: 355
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(355)
; OTHER INFORMATION: n = A,T,C or G
US-09-439-313-401
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Best Local Similarity 99.2%  Pred. No. 1.1e-85;
Matches 352; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 2576 TGATGTCCTCAAGTAGTCACACCTTCATTAACTCTTGAAGCTGTATCATCTTTGCCAAG 2635
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QY 2816 CCCTTTTCATGGCCAAAGTGCATTAACCATGAGCAGCTACTACCATGATGTTCTGC 2870
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Db 301 CCCTTTTCATGGCCAAAGTGCATTAACCATGAGCAGCTACTACCATGATGTTCTGC 355
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Search completed: January 16, 2003, 08:15:11
Job time : 145 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 15, 2003, 17:52:41 ; Search time 4199 Seconds
(without alignments)
13279.605 Million cell updates/sec

Title: US-09-807-201-8

Perfect score: 3443
Sequence: 1 gggcgggcgccggcgagtag.....ctgttcacatggcgctgata 3443

Scoring table: IDENTITY_MUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 segs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

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1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estrov:*
6: em_estropl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
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27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	782.6	22.7	866	13	BI761763 603046751
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4	647.2	18.8	909	12	BG485061 602503876
5	626.4	18.2	639	14	BM784118 K-EST0062
6	583.2	16.9	792	12	BE867224 601442284

7	578.4	16.8	591	14	BM747154 K-EST0021
8	568.4	16.5	639	9	AI989307 36 Prosta
9	553	16.1	553	13	BM126575
10	545	15.8	545	13	BM126828 1e99a04.x
11	540.2	15.7	591	14	BM770321 K-EST0053
12	533	15.5	533	14	BM829557 K-EST0102
13	492	14.3	529	10	AM058537
14	483.8	14.1	487	9	AI660243
15	475.4	13.8	489	9	AI826806
16	467.4	13.6	480	14	BM771081
17	466.8	13.6	814	12	BF675496
18	465	13.5	465	12	BE857738
19	460	13.4	470	10	AM025029
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22	451	13.1	491	12	BF809595
23	446.6	13.0	453	9	AI167953
24	446.4	13.0	450	9	AI393270
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26	446	13.0	500	12	BF736834 QV3-KT001
27	436.2	12.7	486	10	AM660347
28	430.4	12.5	736	13	BI454294
29	423.2	12.3	837	12	BF574140
30	418.4	12.2	429	9	AI289207
31	418.4	12.2	634	14	BM828756
32	417.4	12.1	429	9	AI272714
33	411.2	11.9	521	10	AM660303
34	408.6	11.9	450	12	BF940659
35	408.6	11.9	509	10	AM604978
36	404	11.7	737	12	BF168078
37	402	11.7	944	14	BQ228388
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39	397.6	11.5	416	10	AM996667
40	395.2	11.5	417	9	AI673506
41	395.2	11.5	796	13	BI556978
42	391.2	11.4	528	12	BF076876
43	382.6	11.1	697	13	BI454495
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ALIGNMENTS

RESULT 1
LOCUS AF318374 2394 bp mRNA linear HTC 01-JAN-2002
DEFINITION Homo sapiens PP9284 mRNA, complete cds.
ACCESSION AF318374
VERSION AF318374.1 GI:18027839
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS Jiang,H.Q., Zhou,X.M., Zhang,P.P., Huang,Y., Qin,W.X., Zhao,X.T., Wan,D.F. and Gu,J.R.
TITLE Novel human cDNA clones with function of inhibiting cancer cell growth
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2394)
AUTHORS Jiang,H.Q., Zhou,X.M., Zhang,P.P., Huang,Y., Qin,W.X., Zhao,X.T., Wan,D.F. and Gu,J.R.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-2000) National Laboratory For Oncogenes & Related Genes, Shanghai Cancer Institute, 25/ln 2200 Xie-Tu Road, Shanghai 200032, P. R. China
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/gene="pp284"
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Query Match 45.1%; Score 1551.6; DB 11; Length 2394;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1599; Conservative 0; Mismatches 4; Indels 5; Gaps 4;

OY 1616 GGCACAGGCTAATCCACATGCTTCTGCTTGCACGTCGTTTACAGAAACATGGG 1675
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OY 1676 GCTGTTTGGCTTCCCGGTCATGATTTACTGTAGAGATGATTCAGAGGTCATTTCA 1735
Db 794 GCTGTTTGGCTTCCCGGTCATGATTTACTGTAGAGATGATTCAGAGGTCATTTCA 813
OY 1736 TTTATTAACAGTGAATGCTTGTGCTTGGACATCTGACATTTCTGTGACGCTGCAG 1795
Db 814 TTTATTAACAGTGAATGCTTGTGCTTGGACATCTGACATTTCTGTGACGCTGCAG 873
OY 1796 TGGCTCCCGCTGCGCAGCTGCTCTCCCTAACCCCTTTGTCGCAAGGGTGATGGCCGCT 1855
Db 874 TGGCTCCCGCTGCGCAGCTGCTCTCCCTAACCCCTTTGTCGCAAGGGTGATGGCCGCT 933
OY 1856 GATTGAGGACATGAGCGGTCAGTGTGAGAGAGAGGGGAGGGGTCGCCCATTTGAGATC 1915
Db 934 GATTGAGGACATGAGCGGTCAGTGTGAGAGAGAGGGGAGGGGTCGCCCATTTGAGATC 993
OY 1916 TTTCTGCTGAGTCTTTTCCAGGGGCAATTTTGGATGAGATGAGCTGTCACTCTCAG 1975
Db 994 TTTCTGCTGAGTCTTTTCCAGGGGCAATTTTGGATGAGATGAGCTGTCACTCTCAG 1053
OY 1976 CTGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2035
Db 1054 CTGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1113
OY 2036 CTGACAGGCGCTG-CCTCTGGGGGCACTTGTGTGCTCCGACCTTACCTCTCACAAAGG 2094
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OY 2455 CCTGCTAGTCACTGGAATTTGAGTGCATGGGGAAATCAAGATGCTACGTTTAAGSTA 2514
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OY 2995 GAGCAGCATTTCCAGGACCTTTGGAACAGTTGGACATGTAAGTGTCTGCCCAAGA 3054
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OY 3055 CACATCCATAAAGGTGTGTATGTTGTAAGAAAGTGTCTCTTATTTATGCCCCCTTCTAT 3114
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OY 3115 TTATGTGAACAACCTTGTCTTTTGTATCTTTTGAACCTGAAGTTCAATTTGTG 3174
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OY 3175 AAATGAATATCATGCAAAATTAATATGCGATTTTTCAAAGTAA 3222
Db 2250 AAATGAATATCATGCAAAATTAATATGCGATTTTTCAAAGTAA 2297

RESULT 2

B1761763

LOCUS

DEFINITION

ACCESSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

603046751F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5187060 5',
mRNA sequence.
B1761763
B1761763.1 GI:15753341
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.

Db 480 CTGGAAATTGAGTCCATCGGGGAAATCAAGATGCTCAGTTAAAGCTACACTGTTTCCA 539
 Qy 2526 TGTATGTTTCTACACATGCTACCTCAGTGTCTGTGAAGTCTTTGATGTCTCC 2585
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 mRNA sequence.
 ACCESSION BM784118
 VERSION BM784118.1 GI:19132350
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 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 639)
 Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 JOURNAL Unpublished (2002)
 COMMENT Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong, Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 31 row: F column: 04
 High quality sequence stop: 639.
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 /cell_line="SND-719"
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 /note="Organ: Stomach; Vector: pCNS; Site:1; EcoRI;
 Site2: NotI; The poly (A)+ RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then decapped
 with tobacco acid pyrophosphatase (TAP). The decapped
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dT-selected mRNA by
 priming with dT-tailed vector. The dT-tailed vector was

adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okazaki-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

BASE COUNT 159 a 148 c 176 g 156 t
 ORIGIN

Query Match 18.2%; Score 626.4; DB 14; Length 639;
 Best Local Similarity 99.7%; Pred. No. 4.4e-134;
 Matches 638; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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 Db 301 TGCCAGGCTGACAGTGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 359
 Qy 1518 GGGATATCAAGCTGGGGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1577
 Db 360 GGGATATCAAGCTGGGGGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419
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 Db 540 TGATTTACTCTTGAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 599
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 DEFINITION 601442284F1 NIH_MGC_65 Homo sapiens cDNA clone IMAGE:3846572 5',
 mRNA sequence.
 ACCESSION BE867224
 VERSION BE867224.1 GI:10316000
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 792)

AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: rsb@nih.gov

Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LLM9559 row: g column: 21
 High quality sequence stop: 676.
 Location/Qualifiers

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 Average insert size 1.8 kb. Library constructed by Life
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Query Match 16.9%; Score 503.2; DB 12; Length 792;
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 Matches 640; Conservative 0; Mismatches 3; Indels 5; Gaps 5;

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 OY 1942 AATTTGGATGAGCATGAGTGTACCTCTCAGCTGCTGATGATGAGATGAAAAAG 2001
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 DB 181 AATTTGGATGAGCATGAGTGTACCTCTCAGCTGCTGATGATGAGATGAAAAAG 240
 OY 2002 GAGAGACATGMAAGGAGAGACAGCCAGGTGACCTGCAGCGGGCTG-CCTCTGGGGCCAC 2060
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 DB 241 GAGAGACATGMAAGGAGAGACAGCCAGGTGACCTGCAGCGGGCTG-CCTCTGGGGCCAC 300
 OY 2061 TTGGTAGTGTCCCGACGCTACTCTCCACAAAGGGATTTTGTGTATGGGTTCTTAGAGCC 2120
 |||||||
 DB 301 TTGGTAGTGTCCCGACGCTACTCTCCACAAAGGGATTTTGTGTATGGGTTCTTAGAGCC 360
 OY 2121 TTAGCAGCCCTGATGATGGCCAGAAATTAAGGAGACACGCTTATGGTGGTGAACGTCG 2180
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 DB 361 TTAGCAGCCCTGATGATGGCCAGAAATTAAGGAGACACGCTTATGGTGGTGAACGTCG 420
 OY 2181 GTATGACCTGTGTAAAGGGAAGAAACATTTTGTCTTATGGGTTGAATATAGACA 2240
 |||||||
 DB 421 GTATGACCTGTGTAAAGGGAAGAAACATTTTGTCTTATGGGTTGAATATAGACA 478
 OY 2241 GTGCCCCCTGGGTGCGAAGGAACATTTGAAAAAGAACTTGGCTTAGACACTCTCTGTGCA 2300
 |||||||
 DB 479 GTGCCCCCTGGGTGCGAAGGAACATTTGAAAAAGAACTTGGCTTAGACACTCTCTGTGCA 537
 OY 2301 GGTCTCCACCTGACATTTGGTGGGCTCTCTGGAGGG-AGACTGAGCCTTCTCTCTCAT 2359
 |||||||
 DB 538 GGTCTCCACCTGACATTTGGTGGGCTCTCTGGAGGGAGAAAGACTAGCCTTCTCTCTCAT 597

OY 2360 CCTCCCTGACCTGCTCTCTAGCACCCTTGAGAGTGCACATGCCCTTG 2407
 |||||||
 DB 538 CCTCCCTGACCTGCTCTCTAGCACCCTTGAGAGTGCACATGCCCTTG 645

RESULT 7

LOCUS

DEFINITION

BM747154 591 bp mRNA linear EST 04-MAR-2002
 K-EST0021659 S6SNU620 Homo sapiens cDNA clone S6SNU620-20-F02 5',
 mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2002)
 Contact: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 20 row: F column: 02
 High quality sequence stop: 591.
 Location/Qualifiers

FEATURES

source

1..591
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="S6SNU620-20-F02"
 /clone_lib="S6SNU620"
 /sex="F"
 /tissue_type="Asclites"
 /cell_type="Scattering floating"
 /cell_line="SNU-620"
 /lab_host="Top10F"
 /note="Organ: Stomach; Vector: pCNS; Site_1: EcoRI;
 Site_2: NotI; The poly (A) + RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then dephosphorylated
 with tabacco acid pyrophosphatase (TAP). The dephosphorylated
 intact mRNA was ligated with DNA-RNA linker including EcoR
 I site by treatment of T4 RNA ligase and the first strand
 cDNA was synthesized from oligo dT-selected mRNA by
 priming with dT-tailed vector. The dT-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

BASE COUNT

ORIGIN

Query Match 16.8%; Score 578.4; DB 14; Length 591;
 Best Local Similarity 99.7%; Pred. No. 5.5e-123;
 Matches 590; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 817 AAAAAGTACACAGTGTGCTGTTCTTCAAAAGCAAGTGTCTTACGCTGATAGC 876
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 DB 1 AAAAAGTACACAGTGTGCTGTTCTTCAAAAGCAAGTGTCTTACGCTGATAGC 60
 OY 877 CTGCGGGGTGCACTTGAAGCTCAAGCCGCGAGAGAGATCGTGGGCGCGAGAGCGCCCT 936
 |||||||
 DB 61 CTGCGGGGTGCACTTGAAGCTCAAGCCGCGAGAGAGATCGTGGGCGCGAGAGCGCCCT 120

OY 937 CCCGGGGGCGCCCTGGGGCAGGTCAGCCTGCAGTCAGAACGTCACGTCGCGGAG 996
 DB 121 CCCGGGGGCGCTGGCCCT-GGAGGTCAGCCTGCAGCTCCAGAACGTCACGTCGCGGAG 179
 OY 997 GCTCCATCATCACCACCCCGAGTGATGTCACAGCCGCCACCTGCGTGAGAAAACTCTTA 1056
 DB 180 GCTTCATCATCACCACCCCGAGTGATGTCACAGCCGCCACCTGCGTGAGAAAACTCTTA 239
 OY 1057 ACAATCCATGGCATGGAGCGCATTTGGGGGATTTTGAGACAATGTTTCATGTTCTATG 1116
 DB 240 ACAATCCATGGCATGGAGCGCATTTGGGGGATTTTGAGACAATGTTTCATGTTCTATG 299
 OY 1117 GAGCCGGATACCAAGTAGAAAAAGTATTTTCATCCAAATTAATGACTCCAGACCAAGA 1176
 DB 300 GAGCCGGATACCAAGTAGAAAAAGTATTTTCATCCAAATTAATGACTCCAGACCAAGA 359
 OY 1177 ACAATGACATTTGCGTGATGAGAGCTGTCAGAACGCTCTGCTTCAACGACCTAGTAAAC 1236
 DB 360 ACAATGACATTTGCGTGATGAGAGCTGTCAGAACGCTCTGCTTCAACGACCTAGTAAAC 419
 OY 1237 CAGTGTGTCGCGCAACCCAGCATGATGCTGCAGCCAGAACAGCTCTGCTGATTTCCG 1296
 DB 420 CAGTGTGTCGCGCAACCCAGCATGATGCTGCAGCCAGAACAGCTCTGCTGATTTCCG 479
 OY 1297 GGTGGGGGGCCACGAGGAAAGGAGAACCTCAGAACGCTGGAACGCTGCCAAGGTGC 1356
 DB 480 GGTGGGGGGCCACGAGGAAAGGAGAACCTCAGAACGCTGGAACGCTGCCAAGGTGC 539
 OY 1357 TTCCTATTGACACAGAGATGCAACAGCATATGCTCTATGACAACTGAT 1408
 DB 540 TTCCTATTGACACAGAGATGCAACAGCATATGCTCTATGACAACTGAT 591

RESULT 8
 LOCUS A1989307 639 bp mRNA linear EST 02-SEP-2001
 DEFINITION 36 prostate cancer cell line LNCap Homo sapiens cDNA, mRNA
 sequence.
 ACCESSION A1989307
 VERSION A1989307.1 GI:15421055
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 639)
 ZHANG, J.S. and SMITH, D.I.
 High throughput screening for androgen regulated genes in LNCap
 cells: Identification of hMG-2 as an androgen regulated gene over
 expressed in prostate adenocarcinoma
 Unpublished (1999)
 CONTACT: Zhang, Jin-San
 Dept. Pathology and Lab Medicine
 Mayo Clinic Cancer Center
 200 1st St. SW, Rochester MN 55905, USA
 Tel: 507-2660311
 Fax: 507-2665193
 Email: zhang.jinsan@mayo.edu.

FEATURES

Source

1. 639

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="prostate cancer cell line LNCap"

/cell_line="LNCap"

/note="prostate cancer metastasized to lymph node;
subtracted cDNA libraries from prostate cancer cell line
LNCap treated with androgen."

BASE COUNT 138 a 146 c 182 g 163 t 10 others
 ORIGIN

Query Match 16.5%; Score 568.4; DB 9; Length 639;
 Best Local Similarity 95.0%; Pred. No. 1.1e-120;

Matches 603; Conservative 0; Mismatches 30; Indels 2; Gaps 2;

OY 1573 GGAATGTGATGATTCACAGGACTGATTTATGACAAATAGAGGAGAGCGCTAATCCA 1632
 DB 1 GGAATGTGATGATTCACAGGACTGATTTATGACAAATAGAGGAGAGCGCTAATCCA 60
 OY 1633 CATGCTCTCGTCCCTTGAGCTGCTTTTACAAAGAAACAATGGGGCTGTTTCCCTCC 1692
 DB 61 CATGCTCTCGTCCCTTGAGCTGCTTTTACAAAGAAACAATGGGGCTGTTTCCCTCC 120
 OY 1693 GTGCAATGATTTACTCTTAGAGATGATTCAGAGCTCCTTATTTTATTAACAGTAAAC 1752
 DB 121 GTGCAATGATTTACTCTTAGAGATGATTCAGAGCTCCTTATTTTATTAACAGTAAAC 180
 OY 1753 TTGCTGGCTTTGGACCTGCTCCATTCCTGTCAGAGCTCAGTGGCTCCCGCCAGC 1812
 DB 181 TTGCTGGCTTTGGACCTGCTCCATTCCTGTCAGAGCTCAGTGGCTCCCGCCAGC 240
 OY 1813 CTGCTCTCCCTTAACCCCTTGTCGCAAGGGGTGATGGCCGCTGTTGGGCACTGGCG 1872
 DB 241 CTGCTCTCCCTTAACCCCTTGTCGCAAGGGGTGATGGCCGCTGTTGGGCACTGGCG 300
 OY 1873 GTCAATGTGAGAGAGAGGGGTGGAGCTGCCCATTTAGATCTTCTGCTGATCTTT 1932
 DB 301 GTCAATGTGAGAGAGAGGGGTGGAGCTGCCCATTTAGATCTTCTGCTGATCTTT 360
 OY 1933 CCAGGGGCCAATTTTGGATGAGCATGAGCTGTCACCTGTCAGCTGCTGATGATTTGAG 1992
 DB 361 CCAGGGGCCAATTTTGGATGAGCATGAGCTGTCACCTGTCAGCTGCTGATGATTTGAG 420
 OY 1993 ATGAAAAAGAGAGACATGAGAAAGGAGAGACAGCCAGGTGACCTGCAGCGCTG-CCTC 2051
 DB 421 ATGAAAAAGAGAGACATGAGAAAGGAGAGACAGCCAGGTGACCTGCAGCGCTG 480
 OY 2052 TGGGGCCACTTGTGATGTCCTCCAGCCTACCTCTCCACAAAGGGATTTCTATGAGTT 2111
 DB 481 TGGGGCCACTTGTGATGTCCTCCAGCCTACCTCTTCAACAAAGGGATTTCTATGAGTT 540
 OY 2112 CTTAGAGCCTTAGCAGCCCTGATGTTGGCCAGAAATTAAGGAGACCAAGCCCTCATGGGT 2171
 DB 541 CTTAGAGCCTTAGCAGCCCTGATGTTGGCCAGAAATTAAGGAGACCA-CCCTTATTTGGGT 599
 OY 2172 GGTGACGTGTGACTGACCTTTGTAAGGGGAACAGAA 2206
 DB 600 GGTGACGTGTGACTGACCTTTGTAAGGGGAACAGAA 634

RESULT 9

BM126575/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 535)
 Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,
 Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistein, A.,
 Schmitt, A., Phelps, B., Rutter, E., Ronko, I., Bennett, J., Cardenas,
 M., Gibbons, M., McCann, R., Cole, R., Tsagarashvili, R., Williams, T.,
 Jackson, Y., and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138

Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmellon@biohp.harvard.edu
 Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center for information on
 obtaining a clone please contact: Juliana Brown
 (brownj@fas.harvard.edu) This sequence now available from the IMAGE
 Consortium, for clone orders contact: info@image.llnl.gov
 Seq primer: -400p from GIBCO
 High quality sequence stop: 452.

FEATURES

source

1..553
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5675022"
 /clone_1lb="Melton Normalized Human Islet 4 N4-HIS 1"
 /sex="Both"
 /tissue_type="Islets of Langerhans"
 /dev_stage="Adult"
 /lab_host="DH10B"
 /note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
 Site_2: Sal 1; Starting library constructed using
 SuperScript Plasmid Library kit (Life Technologies). cDNA
 made by oligo-dt priming. Size-selected by column
 fractionation; average insert size 1.08 kb. Library was
 amplified once on solid support and plasmid DNA from
 library was prepared. The library DNA was normalized by
 method #4 from Bonaldo, Lennon, and Soares 1996 Genome
 Research 6:791-806; 0.5 microgram single-stranded library
 plasmid DNA was mixed with 5 micrograms PCR product
 representing library inserts and hybridized to an EcoT of
 20. Single-stranded (unhybridized) plasmids were isolated
 by hydroxyapatite chromatography and used to make this
 library."

BASE COUNT 175 a 121 c 114 g 143 t
 ORIGIN

Query Match 16.18; Score 553; DB 13; Length 553;
 Best Local Similarity 100.0%; Pred. No. 4.1e-117;

Matches 553; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2663 TTGCAAAAATGACGCGCTGACTTACGTTCTTAATGATGCTGAAGCAAAATG 2722
 DB 553 TTGCAAAAATGACGCGCTGACTTACGTTCTTAATGATGCTGAAGCAAAATG 494
 OY 2723 CCATGCTGCGGCGGCAAGAGAAAGATGCTTTTGGACTCTGTGTCCTT 2782
 DB 493 CCATGCTGCGGCGGCAAGAGAAAGATGCTTTTGGACTCTGTGTCCTT 434
 OY 2783 CCATGCTGCGGCTTCCACACGAGGAGGCTCCCTTTGCAATGCCATTAAC 2842
 DB 433 CCATGCTGCGGCTTCCACACGAGGAGGCTCCCTTTGCAATGCCATTAAC 374
 OY 2843 CATGACGACTACTACCATGCTTCTGCTGCGCAAGAGGCTGTTGCAAGAAATG 2902
 DB 373 CATGACGACTACTACCATGCTTCTGCTGCGCAAGAGGCTGTTGCAAGAAATG 314
 OY 2903 AAATGAATGATTTACAGACTTACCTTGAATGAGAAAGTCTTGCATCCCATTT 2962
 DB 313 AAATGAATGATTTACAGACTTACCTTGAATGAGAAAGTCTTGCATCCCATTT 254
 OY 2963 GCAGATCCGCTGTGACATAGCTCTTAAAGACAGCATTTCCAGGACCTTGAAGAC 3022
 DB 253 GCAGATCCGCTGTGACATAGCTCTTAAAGACAGCATTTCCAGGACCTTGAAGAC 194
 OY 3023 AGTTGGACCTTAAGAGTCTTGTCCCAAGACATCTAAAGAGTGTGTAATGATGA 3082
 DB 193 AGTTGGACCTTAAGAGTCTTGTCCCAAGACATCTAAAGAGTGTGTAATGATGA 134
 OY 3083 AAACGCTTCTCTTCTTATATGCCCCCTTATTTATGTAACAACACTGTTGCTTTT 3142
 DB 133 AAACGCTTCTCTTCTTATATGCCCCCTTATTTATGTAACAACACTGTTGCTTTT 74

OY 3143 GTATCTTTTAACTGTAAGTTCATGTAAGAAATGATATCATGCAAAATTAATATG 3202
 DB 73 GTATCTTTTAACTGTAAGTTCATGTAAGAAATGATATCATGCAAAATTAATATG 14
 OY 3203 CGATTTTCTTTC 3215
 DB 13 CGATTTTCTTTC 1

RESULT 10

BM126828

LOCUS 545 bp mRNA linear EST 12-MAR-2002
 DEFINITION l699a04.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
 CDNA clone IMAGE:5675022 5', mRNA sequence.

ACCESSION

BM126828

VERSION

BM126828.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE

1 (bases 1 to 545)

AUTHORS

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,

Lentshka,I., Scarce,M., Brestelli,J., Gradwohl,G., Clifton,S.,

Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,D., Blistain,A.,

Schmitt,A., Theising,B., Ritzer,E., Ronko,I., Bennett,J., Cardenas

M., Gibbons,M., McCann,R., Cole,R., Tsagarashvili,R., Williams,T.,

Jackson,Y. and Bowers,Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Other-ESTs: l699a04.x1

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,

MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmellon@biohp.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:

Washington University Genome Sequencing Center for information on

obtaining a clone please contact: Juliana Brown

(brownj@fas.harvard.edu) This sequence now available from the IMAGE

Consortium, for clone orders contact: info@image.llnl.gov

Seq primer: -400p from GIBCO

High quality sequence stop: 430.

Location/Qualifiers

1..545

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5675022"

/clone_1lb="Melton Normalized Human Islet 4 N4-HIS 1"

/sex="Both"

/tissue_type="Islets of Langerhans"

/dev_stage="Adult"

/lab_host="DH10B"

/note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
 Site_2: Sal 1; Starting library constructed using
 SuperScript Plasmid Library kit (Life Technologies). cDNA
 made by oligo-dt priming. Size-selected by column
 fractionation; average insert size 1.08 kb. Library was
 amplified once on solid support and plasmid DNA from
 library was prepared. The library DNA was normalized by
 method #4 from Bonaldo, Lennon, and Soares 1996 Genome
 Research 6:791-806; 0.5 microgram single-stranded library
 plasmid DNA was mixed with 5 micrograms PCR product
 representing library inserts and hybridized to an EcoT of
 20. Single-stranded (unhybridized) plasmids were isolated
 by hydroxyapatite chromatography and used to make this
 library."

BASE COUNT 143 a 113 c 121 g 168 t

ORIGIN

Query Match	Similarity	15.8%	Score 545	DB 13	Length 545
Best Local Similarity	100.0%	Pred. No. 2.9e-115			
Matches 545	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
QY 2664	TCACAAATGACATGGCTCCCTGACCTTAACGCTCTATAATGAATGCTGTAAGCAAAAGTGC				2723
Db 1	TGACAAATGACATGGCTCCCTGACCTTAACGCTCTATAATGAATGCTGTAAGCAAAAGTGC				60
QY 2724	CCATGCTGGCGCGCAAGAGAAAGATGCTGTTTGGACTCTGTGTCCTTC				2783
Db 61	CCATGCTGGCGCGCAAGAGAAAGATGCTGTTTGGACTCTGTGTCCTTC				120
QY 2784	CAATGCTGGGTTTCCAAACAGGGGAAGGGCCCTTTGATATGSCCAAGGCCATTAAC				2843
Db 121	CAATGCTGGGTTTCCAAACAGGGGAAGGGCCCTTTGATATGSCCAAGGCCATTAAC				180
QY 2844	ATGAGCACTACTCTACCAACATGGTTCCTCCCTGCGCAAGCAGCTGTTCGAAGATGA				2903
Db 181	ATGAGCACTACTCTACCAACATGGTTCCTCCCTGCGCAAGCAGCTGTTCGAAGATGA				240
QY 2904	AATGAATGATTCCTACAGCTAGGACTTAACTTGAATGAAAAGTCTTCAATCCATTTTG				2963
Db 241	AATGAATGATTCCTACAGCTAGGACTTAACTTGAATGAAAAGTCTTCAATCCATTTTG				300
QY 2964	CAGATCCGCTGTGTCGACATGCTCTGTAGAGAGAGAGATTCGCCAGGACCTTGGAAACA				3023
Db 301	CAGATCCGCTGTGTCGACATGCTCTGTAGAGAGAGAGATTCGCCAGGACCTTGGAAACA				360
QY 3024	GTTGGCACTGTAAAGGTGCTTCTCCCAAGACACATCTTAAAGGTGTGTAAAGGTGTA				3083
Db 361	GTTGGCACTGTAAAGGTGCTTCTCCCAAGACACATCTTAAAGGTGTGTAAAGGTGTA				420
QY 3084	AACGTCCTCTTCTTATTTGCCCCCTTCTTATTTATGTAGTAACAACGTTTGTCTTTTTCG				3143
Db 421	AACGTCCTCTTCTTATTTGCCCCCTTCTTATTTATGTAGTAACAACGTTTGTCTTTTTCG				480
QY 3144	TATCTTTTAACTGTAAGTTCATATTTGTAATTAATGTAATATCATGCAATTAATTAATGC				3203
Db 481	TATCTTTTAACTGTAAGTTCATATTTGTAATTAATGTAATATCATGCAATTAATTAATGC				540
QY 3204	GATTT 3208				
Db 541	GATTT 545				

RESULT 11

BM770321

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

591 bp mRNA linear EST 04-MAR-2002

K-EST053749 S6SN0620s1 Homo sapiens cDNA clone S6SN0620s1-19-D05

5', mRNA sequence.

BM770321

BM770321.1 GI:19099936

EST.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 591)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,

Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

Kim,Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

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Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 19 row: D column: 05

High quality sequence stop: 591.

Location/Qualifiers

	source
	1. 591
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="S6SN620s1-19-D05"
	/clone_1id="S6SN620s1"
	/sex="F"
	/tissue_type="Necites"
	/cell_type="Scattering floating"
	/lab_host="Top10F"
	/lab_line="SNU-620"
	/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
	Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
	bacterial alkaline phosphatase (BAP) and then decapped
	with tabacco acid pyrophosphatase (TAP). The decapped
	intact mRNA was ligated with DNA-RNA linker including EcoR
	I site by treatment of T4 RNA ligase and the first strand
	cDNA was synthesized from oligo dt-selected mRNA by
	priming with dr-tailed vector. The dr-tailed vector was
	adjusted to have about 60nt. The cDNA vector was
	circularized with E. coli DNA ligase after digestion of
	EcoRI which site is also included in vector. An RNA strand
	converted to a DNA strand by Okayama-Berg method. The
	obtained cDNA vectors were used for transformation of
	competent cells E. coli Top10F by electroporation method.
	The cDNA libraries constructed by this method are
	full-length enriched cDNA library. After analyzing and
	sequencing about 2,000 ~ 3,000 colonies in original cDNA
	library, the abundant cDNAs were selected and amplified by
	PCR reaction using vector region primer including T7
	promotor as 5' primer and N(dt)14 as 3' primer. The PCR
	products were used as template for synthesis of
	biotinylated single stranded RNA by in vitro transcription
	reaction. The synthesized RNA probes were hybridized with
	antisense single stranded cDNAs prepared from original
	library and incubated with avidin-gel. After removing
	DNA-RNA hybrids by centrifuge, the subtracted cDNA
	libraries were constructed by transformation of the
	remaining DNA into competent cells E. coli Top10F with
	electroporation method."
BASE COUNT	128 a 149 c 169 g 145 t
ORIGIN	
Query Match	15.7% Score 540.2; DB 14; Length 591;
Best Local Similarity	98.7%; Pred. No. 3.8e-114;
Matches 587; Conservative	0; Mismatches 3; Indels 5; Gaps 4;
OY 1999 AAGGAGACACTGGAAAGGAGACAGCCAGCGGTGC-CCTCTGGGCC 2057	
DB 1 AAGGAGAAACATGGAAAGGAGACAGCCAGGTGGCACTGGACGGCTTCCTTGGGGC 60	
OY 2058 CACTTGGTAGTGTCGCCAGCTACCTCCACAAGGGATTGTTGGTGTGA 2117	
DB 61 CACTTGGTAGTGTCGCCAGCTACCTCCACAAGGGATTGTTGGTGTGA 120	
OY 2118 GCCTTAGCACGCCCTGGATGTGGCCAGAATAAAGGACACAGCCCTTATGGGTGTAC 2177	
DB 121 GCCTTAGACAGCCCTGGATGTGGCCAGAATAAAGGACACAGCCCTTATGGGTGTAC 180	
OY 2178 GTGTAGTACACCTCTTAAGGGGAACAAACATTTTTTTCTTATGGGTGAATATAG 2237	
DB 181 GTGTAGTACA-CTGTAAAGGGGAACAGAAACATTTTTTTCTTATGGGTGAATATAG 239	
OY 2238 ACAGTGCCCTTGGGGGCGAGGGAAGCAATTAAGAAAGAACTGGCCCTAGACACCCTGGT 2297	
DB 240 ACAGTGCCCTT-GGTGGCGAGGGAAAGCAATTAAGAAAGAACTGGCCCTAGACACCTCTGT 298	
OY 2298 GCAGGTCTCCACCTGCACATTTGGGTGGGCTCTTGGAGGAGATCATACCTCTCTCC 2357	
DB 299 GCAGGTCTCCACCTGCACATTTGGGTGGGCTCTTGGAGGAGATCATACCTCTCTCC 358	
OY 2358 ATCTCCTCTGACCTGCTCTAGACACCTTGAGAGATGCACATGCCCTTGGTCTGTGGCA 2417	
DB 359 ATCTCCTCTGACCTGCTCTAGACACCTTGAGAGATGCACATGCCCTTGGTCTGTGG--C 416	

QY 2418 GGGGCGCCAGTCTGGACACATGTTGGCTCTTCAGGCGCTGCTAGTCACTGGAAATTGAG 2477
|||||
DB 417 AGGGCGCCAACTGTGGACACATGTTGGCTCTTCAGGCGCTGCTAGTCACTGGAAATTGAG 476
QY 2478 GTCCATGGGGGAAATTCAGAGATGCTCACTTTAAGGTACAGCTTTCCATGTTATTTCT 2537
|||||
DB 477 GTCCATGGGGGAAATTCAGAGATGCTCACTTTAAGGTACAGCTTTCCATGTTATTTCT 536
QY 2538 ACACATGCTACCTCAGTGTCTCTGGAACCTTACCTTTGATGTCCTCAAGTAGT 2592
|||||
DB 537 ACACATGCTACCTCAGTGTCTCTGGAACCTTACCTTTGATGTCCTCAAGTAGT 591
RESULT 12 533 bp mRNA linear EST 06-MAR-2002
BM829557
LOCUS K-EST0102582 S9SNU601 Homo sapiens cDNA clone S9SNU601-59-G07 5',
DEFINITION mRNA sequence.
ACCESSION BM829557
VERSION BM829557.1 GI:19185966
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 533)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 59 row: G column: 07
High quality sequence stop: 533.
Location/Qualifiers
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site:2: XhoI. The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including SfiI
site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized with Superscript II using SfiI
oligo-dT primer. After first strand synthesis, RNA was
degraded by NaOH treatment and cDNA was amplified by PCR
reaction. The PCR products were digested with SfiI and
cloned into DraIII-digested pME18S-FL3 vector. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

BASE COUNT 115 a 126 c 151 g 141 t
ORIGIN
Query Match 15.5%; Score 533; DB 14; Length 533;
Best Local Similarity 100.0%; Pred. NO. 1.7e-112;
Matches 533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1412 ACCAGCATGATCTGTGCGCGGCTTCTCTCAGGGGAGCGTCAATTTCTCCAGGGTGACAG 1471
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DB 61 ACCAGCATGATCTGTGCGCGGCTTCTCTCAGGGGAGCGTCAATTTCTCCAGGGTGACAG 120
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DB 181 GGGTTCGTGCTGTGCGCAAGCTTACAGACAGAGATGTACGGGATGTGATGATTTAC 240
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DB 301 GTCGTTTACAAAGAAACAAATGAGGGGCTGTTTGTCCCGTGCATGATTTACTCTAG 360
QY 1712 AGATGATTCAGAGGTCACTTCAATTTTATTAACAGTGAATGTGTGCTTTGGACACTC 1771
|||||
DB 361 AGATGATTCAGAGGTCACTTCAATTTTATTAACAGTGAATGTGTGCTTTGGACACTC 420
QY 1772 TCTGCAATTCGTGTCAGAGCTGATGAGGCTCCCGTCCAGCGCTGCTTCCTTACCCCTT 1831
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DB 421 TCTGCAATTCGTGTCAGAGCTGATGAGGCTCCCGTCCAGCGCTGCTTCCTTACCCCTT 480
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DB 481 GTCCCAAGGGGTATGAGCGCGGCTGTTGTGGGCACTGCGGTCAAGTGTGA 533
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DEFINITION similar to SW:TM52_HUMAN O15393 TRANSMEMBRANE PROTEASE, SERINE 2 ;,
mRNA sequence.
ACCESSION AM058537
VERSION AM058537.1 GI:5934176
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 529)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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High quality sequence stop: 319.
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RESULT 15
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DEFINITION mRNA sequence.
ACCESSION AI826806 GI:5447477
VERSION AI826806
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 489)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILML at:
www.bio.llnl.gov/bdrrp/image/image.html
Insert Length: 672 Std Error: 0.00
Seq primer: -400P from GIBCO
High quality sequence stop: 480.
location/Qualifiers
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/note="Organ: prostate; Vector: p773d-Pac (Pharmacia)
with a modified polylinker; 1st strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I - o1190(dt) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified p773 vector. Library is normalized, and was
constructed by Bento Soares and M. Fatima Bonaldo."
BASE COUNT 156 a 105 c 101 g 127 t
ORIGIN
Query Match 13.8% Score 475.4; DB 9; Length 489;
Best Local Similarity 99.6%; Pred. No. 3.6e-99;
Matches 487; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
QY 2735 GCGAAGAGAGAGATGTTTGGACTCTGTGTCCTTCCATGCTGTGG 2794
|||||
DB 489 GCGAAGAGAGAGATGTTTGGACTCTGTGTCCTTCCATGCTGTGG 430
QY 2795 GTTTCACACAGGAGGGTCCCTTTGCAATGGCAAGTCCATACCATGAGCATAC 2854
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DB 429 GTTTCACACAGGAGGGTCCCTTTGCAATGGCAAGTCCATACCATGAGCATAC 370
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DB 369 TCTACCATGTTGCTGCTCCCTGGCCAGCAGGCTGTGCAAGAAATGAATGATGATT 310
QY 2915 CTACAGCTAGAGACTTAACCTTGAATGGAAGTCTTGCAATCCCATTTGCA -GGATCCGT 2973
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DB 309 CTACAGCTAGAGACTTAACCTTGAATGGAAGTCTTGCAATCCCATTTGCAAGGATCCGT 250
QY 2974 CTGTGCACATCCCTCTGTAGAGAGACGATTCCAGGAGCCTTGGAACAGTGGCACTG 3033

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DB 249 CTGTGCACATCCCTCTGTAGAGAGCAGCATTCGCCAGGACCTTGGAAACAGTTGGCACTG 190
QY 3034 TAAGTGTCTGTGCTCCCAAGACACATCCTAAAGAGTGTGTAAGGTGAAACGCTTCC 3093
|||||
DB 189 TAAGTGTCTGTGCTCCCAAGACACATCCTAAAGAGTGTGTAAGGTGAAACGCTTCC 130
QY 3094 TTCTTTATTTGCCCTTCTTATTTATGTGACACATGTTTGTCTTTTGTATCTTTT 3153
DB 129 TTCTTTATTTGCCCTTCTTATTTATGTGACACATGTTTGTCTTTTGTATCTTTT 70
QY 3154 AAACGTAAAGTTCATTTGTGAAAAATGAATATCATGCAATAATATATGCAATTTT 3213
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QY 3214 TCAAGTAA 3222
DB 9 TCAAGTAA 1

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Search completed: January 16, 2003, 08:12:59
Job time : 4228 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2003, 18:24:31 ; Search time 1006 Seconds
(without alignments)
1525.969 Million cell updates/sec

Title: US-09-807-201-8
Perfect score: 3443
Sequence: 1 g9gcggccggccgagtag.....ctgttcacatggcgtagata 3443

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 393868 seqs, 222934149 residues

Total number of hits satisfying chosen parameters: 787736

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PC1_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3136.8	91.1	3245	9	US-10-012-896-929 Sequence 929, App
2	3136.8	91.1	3245	9	US-09-895-793-929 Sequence 929, App
3	3136.8	91.1	3245	9	US-09-895-814-929 Sequence 929, App
4	3136.8	91.1	3245	10	US-09-759-143-929 Sequence 929, App
5	3136.8	91.1	3245	10	US-09-780-669-929 Sequence 929, App
6	3136.8	91.1	3245	10	US-09-822-827-929 Sequence 929, App
7	2421	70.3	2486	9	US-09-981-353-22 Sequence 22, App1
8	2309.4	67.1	2479	9	US-10-012-896-894 Sequence 894, App
9	2309.4	67.1	2479	9	US-09-895-793-894 Sequence 894, App
10	2309.4	67.1	2479	9	US-09-895-814-894 Sequence 894, App
11	2309.4	67.1	2479	10	US-09-759-143-894 Sequence 894, App
12	2309.4	67.1	2479	10	US-09-780-669-894 Sequence 894, App
13	2309.4	67.1	2479	10	US-09-822-827-894 Sequence 894, App
14	1464.8	42.5	1479	9	US-10-012-896-930 Sequence 930, App
15	1464.8	42.5	1479	9	US-09-895-793-930 Sequence 930, App
16	1464.8	42.5	1479	9	US-09-895-814-930 Sequence 930, App
17	1464.8	42.5	1479	10	US-09-759-143-930 Sequence 930, App
18	1464.8	42.5	1479	10	US-09-780-669-930 Sequence 930, App
19	1464.8	42.5	1479	10	US-09-822-827-930 Sequence 930, App

20	1461.8	42.5	1476	9	US-10-012-896-931 Sequence 931, App
21	1461.8	42.5	1476	9	US-09-895-793-931 Sequence 931, App
22	1461.8	42.5	1476	9	US-09-895-814-931 Sequence 931, App
23	1461.8	42.5	1476	10	US-09-759-143-931 Sequence 931, App
24	1461.8	42.5	1476	10	US-09-780-669-931 Sequence 931, App
25	1461.8	42.5	1476	10	US-09-822-827-931 Sequence 931, App
26	983	28.6	1077	10	US-09-988-978A-2 Sequence 2, App1
27	681.4	19.8	683	9	US-10-012-896-896 Sequence 896, App
28	681.4	19.8	683	9	US-09-895-793-896 Sequence 896, App
29	681.4	19.8	683	9	US-09-895-814-896 Sequence 896, App
30	681.4	19.8	683	10	US-09-759-143-896 Sequence 896, App
31	681.4	19.8	683	10	US-09-780-669-896 Sequence 896, App
32	681.4	19.8	683	10	US-09-822-827-896 Sequence 896, App
33	490	14.2	557	9	US-10-012-896-384 Sequence 384, App
34	490	14.2	557	9	US-09-895-793-384 Sequence 384, App
35	490	14.2	557	9	US-09-895-814-384 Sequence 384, App
36	490	14.2	557	10	US-09-759-143-384 Sequence 384, App
37	490	14.2	557	10	US-09-780-669-384 Sequence 384, App
38	490	14.2	557	10	US-09-822-827-384 Sequence 384, App
39	398.4	11.6	400	9	US-09-232-880-325 Sequence 325, App
40	398.4	11.6	400	9	US-10-012-896-325 Sequence 325, App
41	398.4	11.6	400	9	US-09-895-793-325 Sequence 325, App
42	398.4	11.6	400	9	US-09-895-814-325 Sequence 325, App
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ALIGNMENTS

RESULT 1
US-10-012-896-929
Sequence 929, Application US/10012896
Publication No. US20020183251A1

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuguu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc A.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick L.
APPLICANT: Wang, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Mantanade, Yoshitiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C27
CURRENT APPLICATION NUMBER: US/10/012, 896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 929
LENGTH: 3245
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-929

Query Match	91.1%;	Score 3136.8;	DB 9;	Length 3245;
Best Local Similarity	99.68;	Pred. NO. 0;		
Matches 3197;	Conservative	0;	Mismatches 7;	Indels 6;
				Gaps 5;

[illegible]

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D	1629	ATGGCTTCGTCCTTGAACGTGTTTTACAAAGAAACATAGGGGCTGTGTTTTGCTTCCCG	1688
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D	1809	TGCTCTCCCTAACCCCTTGTCCGCAAGGGGTGATGTGCCCGGTGTGTGAGCATGCGGG	1868
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D	1929	CAGGGCCCAATTTTGGATGTAGACATGAGAGCTGTCACTCTGCACCTCTGTGATGACTTGAGA	1988
Q	1994	TGAAAAAGAGAGACATGGAAGGAGAGACAGCAGGTGGACCTGCAGAGGGCTG-CTCTCT	2052
D	1989	TGAAAAAGAGAGACATGGAAGGAGAGACAGCAGGTGGACCTGCAGAGGGCTGCCTCT	2048
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D	2049	GGGGCACTGTGTGTGTCCCAAGCCTACCTCTCCAAAGGGGATTTTGTGTGATGGTTTC	2108
Q	2113	TTAGAGCTTATGACAGCCCTGTGATGTGTGCGCAGAAATTAAGGACACAGCCCTTATGGGTG	2172

OY	434	GTGGAGCTGGCGTGGCCCGCTGGCTTACTGTGAAAGTTCTATGGGACGCAAGTGTCTCAAC	493
Db	430	GTGGAGCTGGCGTGGCCCGCTGGCTTACTGTGAAAGTTCTATGGGACGCAAGTGTCTCAAC	489
OY	494	TCTGGAGTAAAGTGCAGACTCCCTCAGGTAAGTATCAACCCCTTAACAGGATGTGTATGC	553
Db	490	TCTGGAGTAAAGTGCAGACTCCCTCAGGTAAGTATCAACCCCTTAACAGGATGTGTATGC	549
OY	554	GTGTACACTGCCCGCGGGGAGAGAAATCGGTTGTTCGCCCTTACGGACCAAC	613
Db	550	GTGTACACTGCCCGCGGGGAGAGAAATCGGTTGTTCGCCCTTACGGATCAAC	609
OY	614	TTCAATCCTTACGGTGTACTCATCTCANAGGAATCCTGGACACCTGTGTGCCAATACAC	673
Db	610	TTCAATCCTTACGGTGTACTCATCTCANAGGAATCCTGGACACCTGTGTGCCAAGCGAC	669
OY	674	TGGAACGAAACTCGGGGCGGGCGCTCGCAGGAGACATGGGCTATTAAGATTAATTTTAC	733
Db	670	TGGAACGAAACTCGGGGCGGGCGCTCGCAGGAGACATGGGCTATTAAGATTAATTTTAC	729
OY	734	TCCTAGCCAGGAATATGTGATGACAGCGGATCCACCAAGCTTTATGAACTGAACACAAGT	793
Db	730	TCCTAGCCAGGAATATGTGATGACAGCGGATCCACCAAGCTTTATGAACTGAACACAAGT	789
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Db	790	GCCGGCAATGTGCAATCTATTAATAAAACCTATACCACAGTATCCGTTCTTCAAAAGCA	849
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Db	850	GTGGTTCTTATACCTGTATATAGCTGGCGGGGTCACTTGAACCTCAAGCCGACGAGACAG	909
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OY	974	CCAGAACCTCCACGCTGTGCGGAGGCTCATCATCACCCCGAGTGGATGTGTCAAGCCGC	1033
Db	969	CCAGAACCTCCACGCTGTGCGGAGGCTCATCATCACCCCGAGTGGATGTGTCAAGCCGC	1022
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Db	1209	GACTTTCAGAGCACTAGTGAACCAGTGTGTGCCCAACCAGGATATGCTGTACGCC	1268
OY	1274	AGAACAGCTGTGCGGAAATTCOCGGGTGGGGGCGACCGAGGAAAGGGAACCACTCAGA	1333
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OY	1334	AGTGTGAACGCTCCAAAGGTGTCTTCATTGAGACACAGAGATGCACAGCAGATATGT	1399
Db	1329	AGTGTGAACGCTCCAAAGGTGTCTTCATTGAGACACAGAGATGCACAGCAGATATGT	1388
OY	1394	CTATATGACAACCTGATTCACACACGCAATGTCTGTCCGCGTTCTCTCAAGGGAAAGTCTGA	1448
Db	1389	CTATATGACAACCTGATTCACACACGCAATGTCTGTCCGCGTTCTCTCAAGGGAAAGTCTGA	1444
OY	1454	TTCTTGGCAGGAGTACAGTGGAGGGCCTGTGTACCTTGGAAGAACAAATATCTGGTGGCT	1511
Db	1449	TTCTTGGCAGGAGTACAGTGGAGGGCCTGTGTACCTTGGAAGAACAAATATCTGGTGGCT	1506

QY	1514	GAAGGGATTAACAGCTGGGGTTCTGGCTGTGCCAAAGCTTCAACACAGAGGTATAGG	1573
Db	1509	GAATAGGGATTAACAGCTGGGGTTCTGGCTGTGCCAAAGCTTCAACACAGAGGTATAGG	1568
QY	1574	GAATGGAATGATTCACAGCACTGATATTATGACAAATGAGGGAGAGAGCGTAAATCAC	1633
Db	1569	GAATGGAATGATTCACAGCACTGATATTATGACAAATGAGGGAGAGAGCGTAAATCAC	1628
QY	1634	ATGGTCCTTCGCTTCGACGTCGTTTTACAGAAAAACAATGGGGCTGTTTTGCTTCCCG	1693
Db	1629	ATGGTCCTTCGCTTCGACGTCGTTTTACAGAAAAACAATGGGGCTGTTTTGCTTCCCG	1688
QY	1694	TGCATGATTTACTCTTAAGAGATTCAGAGCTCACTTCATTTTATTAACAGTAACT	1753
Db	1689	TGCATGATTTACTCTTAAGAGATTCAGAGCTCACTTCATTTTATTAACAGTAACT	1748
QY	1754	TGCTTGCGCTTTGGACACTCTGCTCCATTCTGTGCAGAGCTGCAGTGGCTCCCGCCAGCC	1813
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QY	1814	TGCTCTCCCTAACCCCTTCGTCCGCAAGGGGTGATGGCGGCTGTTTGTGGGCACTGGCGG	1873
Db	1809	TGCTCTCCCTAACCCCTTCGTCCGCAAGGGGTGATGGCGGCTGTTTGTGGGCACTGGCGG	1868
QY	1874	TCAAGTGTGAGAGAGAGGGGTGGAGGCTGCCCATTTAGATTTCTCGTGTAGTCCTTTC	1933
Db	1869	TCAAGTGTGAGAGAGAGGGGTGGAGGCTGCCCATTTAGATTTCTCGTGTAGTCCTTTC	1928
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QY	2233	TATAGACATGCTCTTGGGTGGGAGGAAACAATTGAAAAGAACTTGCCCTGAGCACTC	2292
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QY	2353	TGCTCATCTCCCTGACCTGTCTCTAGCAGCCCTGGAGAGTGCACATGCGCCCTTGCTCT	2412
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QY	2413	GGGACAGGGGCGCAAGTGTGGACCAATGTTGGCTCTTCAAGGCGCTAGTCACTGGAAA	2472
Db	2407	GG--CAGGGCGCAAGTGTGGACCAATGTTGGCTCTTCAAGGCGCTAGTCACTGGAAA	2464
QY	2473	TTTGAGTGTCCATGGGGAAATCAAGGATGCTCAAGTTTAAGGTACACTGTTTCCATGTTATG	2532
Db	2465	TTTGAGTGTCCATGGGGAAATCAAGGATGCTCAAGTTTAAGGTACACTGTTTCCATGTTATG	2524
QY	2533	TTTTCTACACATTTGTAACCTGCAGTGTGCCGCGGAAACCTTATGCTATGCTCCAAATGAT	2592
Db	2525	TTTTCTACACATTTGTAACCTGCAGTGTGCCGCGGAAACCTTATGCTATGCTCCAAATGAT	2584
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Oy	2653	TTACAGTCCTTTGACAAATGACTGCGCTCTGACTTAAAGTTATVAAATGATGTGCTG	2712
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Oy	2893	TGCAAGAATGAATGATGATTTCTACAGCTAGGACTTAACTTGAATGGAAGTCTTGC	2952
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Oy	2953	AATCCCATTTGCGAGATCCGCTGTGTCACATGCTCTGTAGAGACACACTTCCACAGGA	3012
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Oy	3133	GTCCTTTTGTATCTTTTAACTGTAAAGTTCAATGTGAAGTAATATATATGCA	3192
Db	3125	GTCCTTTTGTATCTTTTAACTGTAAAGTTCAATGTGAAGTAATATATATGCA	3184
Oy	3193	ATAAATTATGCGATTTTTTTTTTAAAGTAA	3222
Db	3185	ATAAATTATGCGATTTTTTTTTTAAAGTAA	3214

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RESULT 3
US-09-895-814-929
? Sequence 929, Application US/09895814
? Publication No. US20020193296A1
? GENERAL INFORMATION:
? APPLICANT: Xu, Jiangchun
? APPLICANT: Dillon, Davin C.
? APPLICANT: Mitcham, Jennifer L.
? APPLICANT: Harlocker, Susan L.
? APPLICANT: Jiang, Yugu
? APPLICANT: Kalos, Michael D.
? APPLICANT: Retter, Marc W.
? APPLICANT: Stolk, John A.
? APPLICANT: Day, Craig H.
? APPLICANT: Vedvick, Thomas S.
? APPLICANT: Carter, Darlick
? APPLICANT: Li, Samuel X.
? APPLICANT: Wang, Aijun
? APPLICANT: Skelky, Vasil A.W.
? APPLICANT: Hepler, William T.
? APPLICANT: Henderson, Robert A.
? APPLICANT: Hural, John
? APPLICANT: McNeill, Patricia D.
? APPLICANT: Houghton, Raymond L.
? APPLICANT: Vinals de Bassols, Carlota
? APPLICANT: Foy, Teresa
? APPLICANT: Fanger, Gary R.
? TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
? TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

```

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: FILE REFERENCE: 210121.427C26
: CURRENT APPLICATION NUMBER: US/09/895,814
: CURRENT FILING DATE: 2001-06-29
: NUMBER OF SEQ ID NOS: 990
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 929
: LENGTH: 3245
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-895-814-929

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Query Match	91.1%;	Score 3136.8;	DB 9;	Length 3245;
Best Local Similarity	99.6%;	Pred. No. 0;		
Matches 3197;	Conservative 0;	Mismatches 7;	Indels 6;	Gaps 5

[illegible]

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Dh 910 ATTGTGGCGGCGAGAGCGGCTCCGGGGGCTTGCCCT - GGCAGGTCAAGCTTGACAGT 968
Qy 974 CCAGACGTCACAGTGTGCGGAGGCTCCATCATCACCCGAGTGGATCTGTACAGCCGC 1033
Dh 969 CCAGAACGTCACAGTGTGCGGAGGCTCCATCATCACCCGAGTGGATCTGTACAGCCGC 1028
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Qy 1094 GAGACAAATCTTCAATGTTCTATGAGCGGAGTACCAAGTAAACAAAAGTATTTCTATCC 1153
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Qy 1214 GACTTTCAAGACCTAGTGAACCAAGTGTGTCTGCGCCCAACCCAGGACATGCTGACAGC 1273
Dh 1209 GACTTTCAAGACCTAGTGAACCAAGTGTGTCTGCGCCCAACCCAGGACATGCTGACAGC 1268
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Dh 1329 AGTGTCAAGCTCTGCCAAGTGTCTTCTATGAGACACAGAGATGCAACAGACATATGT 1388
Qy 1394 CTATGACAAACCTGATCAACACAGCATGCTGTGCGGGTCTCCGCGAGGGGAAAGCTGA 1453
Dh 1389 CTATGACAAACCTGATCAACACAGCATGCTGTGCGGGTCTCCGCGAGGGGAAAGCTGA 1448
Qy 1454 TTCTTCCAGGGGTGACATGAGAGGCTCTGTGCTCACTTCAAGAACATATCTGGTGCT 1513
Dh 1449 TTCTTCCAGGGGTGACATGAGAGGCTCTGTGCTCACTTCAAGAACATATCTGGTGCT 1508
Qy 1514 CATAGGGATCAAGAGTGGGTTCTGCTGTGCCAAGCTTACAGACAGAGATGTACGG 1573
Dh 1509 CATAGGGATCAAGAGTGGGTTCTGCTGTGCCAAGCTTACAGACAGAGATGTACGG 1568
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Dh 1629 ATGCTCTCGTCTGACGCTGTTTACAGAAAAACAATGGGGCTGTTTGTGCTCCCG 1688
Qy 1694 TGCATGATTTACTCTTAAAGATGATTCAGAGTCACTTATTTTATTAACAGTGAAT 1753
Dh 1689 TGCATGATTTACTCTTAAAGATGATTCAGAGTCACTTATTTTATTAACAGTGAAT 1748
Qy 1754 TGTCTGGCTTGGGACCTCTGCAATCTGTGAGAGGTGAGTGGCTCCCGTCCAGACG 1813
Dh 1749 TGTCTGGCTTGGGACCTCTGCAATCTGTGAGAGGTGAGTGGCTCCCGTCCAGACG 1808
Qy 1814 TGTCTCTCCCTAACCCCTTGTCCGCAAGGGGATGATGGCGGCTGTTTGGGACAGTGGCG 1873
Dh 1809 TGTCTCTCCCTAACCCCTTGTCCGCAAGGGGATGATGGCGGCTGTTTGGGACAGTGGCG 1868
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Qy 1934 CAGGGGCCAATTTTGGATGAGATGAGAGTGTACCCCTCAGCTGCTGGATGACTTGGA 1993
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Qy 1994 TGAAGAGAGAGACATGGAAGAGAGACCCAGGTGGACCTTGACAGCGGCTG - CTTCT 2052
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RESULT 4
US-09-759-143-929
; Sequence 929, Application US/09759143
; Patent No. US20020022248A1

```

APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Reltter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darlick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS OF AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427023
CURRENT APPLICATION NUMBER: US/09/7759,143
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 929
LENGTH: 3245
TYPE: DNA
ORGANISM: Homo sapiens
US-09-759-143-929

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Query Match	91.1%;	Score	3136.8;	DB	10;	Length	3245;
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Matches 1997; Conservative	0;	Mismatches	7;	Indels	6;	Gaps	5;

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Db	1029	CCACTGCGTGGAAAAACCTTTAAACAATCCATGGCAATTGAGCGCAATTTGCGGGGATTTT	1088
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Db	1089	GAGACATCTTTCAATGTTCTATATGAGCGCGGATACCAAGTAGAAAAAGTATTTCTCATCC	1148
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Db	1149	AAATTAATGACTCCAAAGCAACAATGATCATTTGGCTGATGAAGCTCCAGAACCTCT	1208
Oy	1214	GACTTCAAGCACTAGTGAAGCAAGTGTCTGCCAACCCAGGCAATGATGCTGCACCC	1273
Db	1209	GACTTCAAGCACTAGTGAAGCAAGTGTCTGCCAACCCAGGCAATGATGCTGCACCC	1268
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Db	1269	AGAACAGCTGTCTGTGATTTCCGGGTGTGGGGCCACCGAGAGAAAGGAGACCTCAGA	1328
Oy	1334	AGTGTGAACGCTCCCAAGGTCCTCATTTGAGACAGAGATGCAACAGCAGATATGT	1393
Db	1329	AGTGTGAACGCTCCCAAGGTCCTCATTTGAGACAGAGATGCAACAGCAGATATGT	1388
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Db	1389	CTATGACAAACCTATATACACACACCACTGATCTGTGGCGGCTTCTGACAGGGAAAGCTGA	1448
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QY	1574	GAATGTGATGTATTCACGAGCACTGATTTTATCGACAAATAGAGGGACAGCGCTAATCCAC	1633
Db	1569	GAATGTGATGTATTCACGAGCACTGATTTTATCGACAAATAGAGGGACAGCGCTAATCCAC	1628
QY	1634	ATGGTCTCTTGCTCCTTGACAGCTGTTTTCACAAAGAAACATGGGGCTGTGTTTGCTTCCCG	1693
Db	1629	ATGGTCTCTCTTGCTGACAGCTGTTTTCACAAAGAAACATGGGGCTGTGTTTGCTTCCCG	1688
QY	1694	TGCATGATTTACCTTTAGAGATATTCACAGAGGCACCTCATTTTATTAACAGTGAAC	1753
Db	1689	TGCATGATTTACCTTTAGAGATATTCACAGAGGCACCTCATTTTATTAACAGTGAAC	1748
QY	1754	TGCTCTGCTTTGGCACCTCTTGCCACTTCTGTGACAGCTGCACTGGCTCCCTGGCCACGC	1813
Db	1749	TGCTCTGCTTTGGCACCTCTTGCCACTTCTGTGACAGCTGCACTGGCTCCCTGGCCACGC	1808
QY	1814	TGCTCTCTCCCTAACCCCTTGTCTGCGCAAGGGGTGATGGCCGGCTGTGTGGGCATGCGCG	1873
Db	1809	TGCTCTCTCCCTAACCCCTTGTCTGCGCAAGGGGTGATGGCCGGCTGTGTGGGCATGCGCG	1868
QY	1874	TCAAGTGTGGAGGAGAGGGGTGAGAGGCTGCCCATTTGANAATCTCTGCTGAGTCCCTTC	1933
Db	1869	TCAAGTGTGGAGGAGAGGGGTGAGAGGCTGCCCATTTGANAATCTCTGCTGAGTCCCTTC	1928
QY	1934	CAGGGGCCAATTTTGGATGAGCTATGAGAGCTGTACACTCTCAGACTCTGATGACTTGGAGA	1993
Db	1929	CAGGGGCCAATTTTGGATGAGCTATGAGAGCTGTACACTCTCAGACTCTGATGACTTGGAGA	1988
QY	1994	TGAAAAAGAGAGACATGGAAGGAGAGACGCCAGGTGGCACCTGACAGCGCTG-CCTCT	2052
Db	1989	TGAAAAAGAGAGACATGGAAGGAGAGACGCCAGGTGGCACCTGACAGCGCTGCTCTCT	2048
QY	2053	GGGGGCCACTTGGTAGTGTCTCCCGAGCTTACTCTCCACAAAGGGGATTTTGTGATGGGTTC	2112
Db	2049	GGGGGCCACTTGGTAGTGTCTCCCGAGCTTACTCTCCACAAAGGGGATTTTGTGATGGGTTC	2108
QY	2113	TTAGAGCCTTAGAGAGCCTTGATGTGTGGCCAGAAATTAAGGAGACAGCCCTTCATGGGTG	2172
Db	2109	TTAGAGCCTTAGAGAGCCTTGATGTGTGGCCAGAAATTAAGGAGACAGCCCTTCATGGGTG	2168
QY	2223	TATAGACAGTGGCCCTTGTGGGTGCGAGGGGAAGCAATTGAAAAGAACTTGGCCTGAGCACTC	2292
Db	2228	TATAGACAGTGGCCCTTGTGGGTGCGAGGGGAAGCAATTGAAAAGAACTTGGCCTGAGCACTC	2286
QY	2293	CTGTGTGAGAGCTTCACACTTCACATTTGGGGGGGCTCTGGGAGGAGAACTCAGCCTTCC	2352
Db	2287	CTGTGTGAGAGCTTCACACTTCACACTTTGGGTGGGGCTCTCTGGGAGGAGAACTCAGCCTTCC	2346
QY	2353	TCTCATCTCTCCCTGAGCCCTGCTCTAGCACCTGTGAGAGTGCACATGCCCTTGGTGTCT	2412
Db	2347	TCTCATCTCTCCCTGAGCCCTGCTCTAGCACCTGTGAGAGTGCACATGCCCTTGGTGTCT	2406
QY	2413	GGGCGAGGGGGCCCAAGTCTTGGCACCATTTGGGCTCTTAGGGCTGTCTAATCTGAGAA	2472
Db	2407	GG--CAAGGGGGCCCAAGTCTTGGCACCATTTGGGCTCTTAGAGCCTGTGATCTAGTGA	2464
QY	2473	TTTGAGGTCCATGGGGGAAATCAAGGATGCGCATGTTTAAGGTACACGTTCATCTTATG	2532
Db	2465	TTTGAGGTCCATGGGGGAAATCAAGGATGCTCAAGTTCATGAGTACACTGTTCATCTTATG	2524

[illegible]

RESULT 5
US-09-780-669-929
; Sequence 929, Application US/09780669
; Patent No. US20020051977A1
; General Information

; GENERAL INFORMATION

APPLICANT: Xu, Ji

APPLICANT: DILLON

APPLICANT: Mitcha

APPLICANT: Harlow

APPLICANT: Tian

REFLECTION: Young,

APPLICANT: HENDERSON

APPLICANT: Kalos,

APPLICANT: Fanger

APPLICANT: Retter

APPLICANT: Stolk,

APPLICANT: DAY: 0

APPLICANT: Vedvic

ADDITIOAL: Cost of

APPLICANT: CALEB

APPLICANT: Lt. Sa

APPLICANT: Wang,

APPLICANT: Skeiky

APPLICANT: Herjert

APPLICANT: Rural

/s/ [Signature] : 2007-09-18

[illegible]

OY	3013	CCTTGGAAACAGTTGCGACTGTGAAGTGCTTCGCCAAGAAGCAATCTTAAGAAGTGT	3072
Db	3005	CCTTGGAAACAGTTGCGACTGTGAAGTGCTTCGCCAAGAAGCAATCTTAAGAAGTGT	3064
OY	3073	GMAATGTAAGAAACGTCCTCCTCTTTATTATTTAGCCCTCTTATTATTTAGAACACCTGTTT	3132
Db	3065	GTAATGGTAAGAAACGTCCTCCTCTTTATTATTTAGCCCTCTTATTATTTAGAACACCTGTTT	3124
OY	3133	GTCCTTTTTTGTACCTTTTTTTAAAGTGCATAATTGCAAAATGAAATATCATTCGCA	3192
Db	3125	GTCCTTTTTTGTACCTTTTTTTAAAGTGCATAATTGCAAAATGAAATATCATTCGCA	3184
OY	3193	ATAAATTATGCGATTTTTTTTTCCAAGTAA	3222
Db	3185	ATAAATTATGCGATTTTTTTTTCCAAGTAA	3214
RESULT 6			
US-09-822-827 -929			
Sequence 929, Application us/09822827			
Patent No. US20020081680A1			
GENERAL INFORMATION:			
APPLICANT: Xu, Jiangchun			
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND			
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER			
CURRENT APPLICATION NUMBER: US/09/822,827			
NUMBER OF SEQ ID NOS: 982			
SOFTWARE: FastSeq for Windows Version 3.0			
SEQ ID NO 929			
LENGTH: 3245			
TYPE: DNA			
ORGANISM: Homo sapiens			
US-09-822-827 -929			
Query Match			
Best Local Similarity 91.1%; Score 3136.8; DB 10; Length 3245;			
Matches 3197; Conservative 0; Mismatches 7; Indels 6; Gaps 5;			
OY	14	CGAGTAGGCCGCGAGCTAAGCAGAGAGCGCGAGCGCGAGAGCGCGAGCGCGGAGC	73
Db	10	CGCGTCCGCGAGCTAAGCAGAGAGCGCGAGCGCGAGCGCGAGCGCGGAGC	69
OY	74	GCCGCGTGAGCGCGCGAGCTCATTTGAAACATTTCCAGATACCTATCATTTACTGATGCT	133
Db	70	GCCGCGTGAGCGCGCGAGCTCATTTGAAACATTTCCAGATACCTATCATTTACTGATGCT	129
OY	134	GTTGATTAACAGCAGATGAGCTTTGAACTCAGGGTACACACCAGCTATTGACCTTACTAT	193
Db	130	GTTGATTAACACCAAGATGAGCTTTGAACTCAGGGTACACACCAGCTATTGACCTTACTAT	189
OY	194	GAAAACCATGATATCCAACCCGAAAAACCCCTATATCCCGACAGCCCCAATGTGTCCCACCT	253
Db	190	GAAAACCATGATATCCAACCCGAAAAACCCCTATATCCCGACAGCCCCAATGTGTCCCACCT	249
OY	254	GTCCTAGAGTGTCATCCGCGCTCAGTACTACCGGTCCCGCGTCCCGCAGTAGCGCCGAGG	313
Db	250	GTCCTAGAGTGTCATCCGCGCTCAGTACTACCGGTCCCGCGTCCCGCAGTAGCGCCGAGG	309
OY	314	GTCCTAGCAGCAGGCTTCCAAACCCCGGTGTCTGACGACGAGCCCAAATCCCATCCGGGACA	373
Db	310	GTCCTAGCAGCAGGCTTCCAAACCCCGGTGTCTGACGACGAGCCCAAATCCCATCCGGGACA	369
OY	374	GTCGTACACCTAAGAAAGCTAAAGAAAGCACTGTGTCATCACCCTTGAGCCCTGGGACCTTCTC	433
Db	370	GTCGTACACCTAAGAAAGCTAAAGAAAGCACTGTGTCATCACCCTTGAGCCCTGGGACCTTCTC	429
OY	434	GTCGAGAGCTGGCGTGGCCGCTGAGCTTACTCTGGAAGTTCAATGGGCGAGAAGTGTCTCAAC	493
Db	430	GTCGAGAGCTGGCGTGGCCGCTGAGCTTACTCTGGAAGTTCAATGGGCGAGAAGTGTCTCAAC	489

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Db 490 TCTGGGATAGAGTGAGCTCTCAGTACCTGATCAACCCCTTAACTGGGTATGCG 549
QY 554 GTGTACACTGCCCCGGGGGAGAGAGAGATCGGTGTTGCGCTTACGGACCAAC 613
|||||
Db 550 GTGTACACTGCCCCGGGGGAGAGAGAGATCGGTGTTGCGCTTACGGACCAAC 609
QY 614 TTCACTCTTCAAGTGTACTCATCTCAGAGAGAGTCTGACACCTGTGTGCCAAGCAGC 673
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QY 674 TGGAAACGAACTACGGGCGGGCGGCTGACAGGACATGGGCTATAAGATAATTTTAC 733
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Db 730 TCTAGCCAAAGAAATAGTATGATAGACGGGATCCACAGCTTTATGAACTGAACCAAGT 789
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Db 790 GCCGGCAATGTGATATCTATATAAAACTGTACACAGTATGCCCTGTTCTTCAAAAGCA 849
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QY 1094 GAGACAACTCTTCAATGTTCTATGAGCCGAGATACCAAGTAAAGAAAGTATTTTCATCC 1153
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QY 1154 AAATATATGACTCAAGACCAAGAACATGACATGCGCTGATGAAGCTGCAGAACGCTCT 1213
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Db 1209 GACTTTCAACGACCTAGTGAAGAAACGATGTGTGCCCAACCCAGGATGATGCTGCAGCC 1268
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Db 1269 AGAACAGCTGTGCTGATTTCCGGGTGGGGGCGACCCGAGGAAAGGAAACCTCAGA 1328
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Db 1509 GATAGGGATACAAAGCTGGGGTCTGCGTGTGCCAAAGCTTACAGACAGAGTGTACGG 1568
QY 1574 GAATGTGATGTATTCACAGGACTGATTTATGACAAATGAGGCGAGCGCTAATCCAC 1633
|||||

Db 1569 GAATGTGATGTATTCACAGGACTGATTTATCGACAAATGAGGCGAGCGCTAATCCAC 1628
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Db 1689 TGCATGATTTTACTTTAGAGATGATTCAGAGGTCACTTCAATTTTATTAACAGTMACT 1748
QY 1754 TGTGTGCTTTGGCACTCTCTGCAATTTGTGTGAGGCTGCACTGCTCCCTGCCAGCC 1813
Db 1749 TGTGTGCTTTGGCACTCTCTGCAATTTGTGTGAGGCTGCACTGCTCCCTGCCAGCC 1808
QY 1814 TGTCTCCCTTAACCCCTTTCGCGCAAGGGGTGATGAGCGGCTGTGTGGGCACTGGCG 1873
Db 1809 TGTCTCCCTTAACCCCTTTCGCGCAAGGGGTGATGAGCGGCTGTGTGGGCACTGGCG 1868
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Db 1929 CAGGGGCCAATTTTGGATGATGATGAGTGTACCTCTCAGTGTGATGACTTGA 1988
QY 1994 TGAAGAGAGAGAGATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2052
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Db 2347 TCCCTATCCCTGACCTGCTGCTAGCAGCCCTGAGAGAGTGAATGAGAGAGAGAGAGAG 2406
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Db 2407 GG--CAGGGCGGCAAGTGTGCGACATGTTGGCTTTCAGGCTGCTAGTACTGAAA 2464
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Db 2585 CCACCTTCAATTTAACTCTTGAAGTGTATCATCTTTGCAAGTAAGAGTGTGGCTAT 2644
QY 2653 TTAGCTGCTTTGACAAATGAGTGTGCTGCTGACTTAAAGTGTGATGATGATGCTG 2712
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 Db 1260 TGATGCTCAGCAGCAGACAGACTCTGTGATTTCCGGGTGGGGGGCCACCGAGAGAAAG 1319
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 Db 1320 GGAAGACCTCAGAAAGTGTGAACGCTGCCAAGGTGCTTCTCATTTGAGACACAGAGATGCA 1379
 Qy 1381 ACAGCAGATATGCTATGACAACTGATCACACGACCATATGATGCTGCGGCTTCTCTGC 1440
 Db 1380 ACAGCAGATATGCTATGACAACTGATCACACGACCATATGATGCTGCGGCTTCTCTGC 1439
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 Db 1440 AGGGGAACGTCGATTTCTGCCAGGGGTGACAGTGAAGGGCTCTGTCTCATCTTGAGAAACA 1499
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 Qy 1621 ACGGCTAAATCCACATGATGCTTCTGCTGACGCTGCTTTTACAAAGAAACATGAGGGCTG 1680
 Db 1620 ACGGCTAAATCCACATGATGCTTCTGCTGACGCTGCTTTTACAAAGAAACATGAGGGCTG 1679
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 Db 1680 TTTTTCCTTCCCGCTGATGATTTACTCTTGAAGATGATTCAGAGTCACTTCAATTTTAT 1739
 Qy 1741 TAAACAGTGAATTTGTGCGCTTTGCGACCTCTGCAATTTGTGCGAGGCTGAGGGCT 1800
 Db 1740 TAAACAGTGAATTTGTGCGCTTTGCGACCTCTGCAATTTGTGCGAGGCTGAGGGCT 1799
 Qy 1801 CCCCTGCCAGCCTCTCTCCCTAACCCCTTGTCCGCAAGGGGTGATGAGCCGGCTGTTG 1860
 Db 1800 CCCCTGCCAGCCTCTCTCCCTAACCCCTTGTCCGCAAGGGGTGATGAGCCGGCTGTTG 1859
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 Qy 1921 GCTGATCCTTTCCAGGGGCCAATTTTGGATGAGCATGAGGTGTCACCTCAGTGTCT 1980
 Db 1920 GCTGATCCTTTCCAGGGGCCAATTTTGGATGAGCATGAGGTGTCACCTCAGTGTCT 1979
 Qy 1981 GGATGACTTGAATGAAAAAGAGAGACATGGAAGGAGAGACAGCCAGGTGACCTGCA 2040
 Db 1980 GGATGACTTGAATGAAAAAGAGAGACATGGAAGGAGAGACAGCCAGGTGACCTGCA 2039
 Qy 2041 GCGGCTG-CCTCTGGGGCCACTTGTGATGTCCCAAGCCTCTCTCCAAAGGGGATTT 2099
 Db 2040 GCGGCTGCTCTGGGGCCACTTGTGATGTCCCAAGCCTCTCTCCAAAGGGGATTT 2099
 Qy 2100 TGGCTATGGGTCTTAGAGCCTTAGACGCCCTGATGCTGGGCGCAGAAATTAAGGAGCCAG 2159
 Db 2100 TGGCTATGGGTCTTAGAGCCTTAGACGCCCTGATGCTGGGCGCAGAAATTAAGGAGCCAG 2159
 Qy 2160 CCGTTCATGGGTGTGAGCTGTAGTCACTTGTAAAGGGAGACAGAAACATTTTGTCT 2219
 Db 2160 CCGTTCATGGGTGTGAGCTGTAGTCACTTGTAAAGGGAGACAGAAACATTTTGTCT 2218
 Qy 2220 TATGGGGTGAATATPAGACAGTGGCTTGGGTGCGAGGGAACAAATTGAAAGAACTT 2279
 Db 2219 TATGGGGTGAATATPAGACAGTGGCTTGGGTGCGAGGGAACAAATTGAAAGAACTT 2277
 Qy 2280 GCCCTGAGACACTCTGCTGAGGCTGCTCCACCTGACATTTGGGGGCTCCGAGGGGA 2339
 Db 2278 GCCCTGAGACACTCTGCTGAGGCTGCTCCACCTGACATTTGGGGGCTCCGAGGGGA 2337

Qy 2340 GACTAGCCTTCTCTCTCATCTCTGACCCCTGCTAGACCCCTGGAGACTGCACAT 2399
 Db 2338 GACTAGCCTTCTCTCTCATCTCTGACCCCTGCTAGACCCCTGGAGACTGCACAT 2397
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 Db 2398 GCCCTTGGTCTCTGGGCGAGGGGCGCCAAAGTGTGGACACATGTTGGCTTTCAGGGCTGC 2455
 Qy 2460 TAGTCACTGGAATTTAGGTTCCATGGGGGA 2490
 Db 2456 TAGTCACTGGAATTTAGGTTCCATGGGGGA 2486

RESULT 8
 US-10-012-896-894
 ; Sequence 894, Application US/10012896
 ; Publication No. US20020183251A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuguu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skelky, Yasir A.W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Hurel, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals de Bassols, Carlota
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Manfande, Yoshihiro
 ; APPLICANT: Meagher, Madeleine Joy
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.427C27
 ; CURRENT APPLICATION NUMBER: US/10/012, 896
 ; NUMBER OF SEQ ID NOS: 1011
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 894
 ; LENGTH: 2479
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-10-012-896-894

Query Match 67.1%; Score 2309.4; DB 9; Length 2479;
 Best Local Similarity 98.6%; Pred No. 0;
 Matches 2425; Conservative 0; Mismatches 21; Indels 13; Gaps 9;

Qy 93 GTCATATGAACATTCACATACCTATCATTTACTGATGCTGTTGATTAACAGCAAGATG 152
 Db 1 GTCATATGAACATTCACATACCTATCATTTACTGATGCTGTTGATTAACAGCAAGATG 60
 Qy 153 CTTTGAATCAGGGTACACACAGCTATTTGAGCTTACTATGTAAGAAACATGATATACAC 212
 Db 61 CTTTGAATCAGGGTACACACAGCTATTTGAGCTTACTATGTAAGAAACATGATATACAC 120
 Qy 213 CGAAACCCCTATCCCGACAGACCCACATGTGTCCCACTGCTACAGAGGTGATCCGG 272
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 Qy 273 CTCAGTACACCCGTCGCCCGTGGCCAGTAGCCGCCGAGGGTCTGACGAGGCTTCCA 332

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Db 181 CTCAGTACTACCCGCTCCCGCCGAGTACGCCCGGAGGGCTCTGACGAGGCTTCCA 240
QY 333 ACCCGGTCGTGACGACGAGCCCAATCCCATCCGAGACAGTGTGACCTCAAGACTA 392
Db 241 ACCCGGTGTGTGACGAGGAGCCCAATCCCATCCGAGACAGTGTGACCTCAAGACTA 300
QY 393 AGAAGACATGTGTGACATCACTTGAACCTTGGGACCTTCTGTGTGGAGCTGCGTGGCG 452
Db 301 AGAAGACATGTGTGACATCACTTGAACCTTGGGACCTTCTGTGTGGAGCTGCGTGGCG 360
QY 453 CTGGGCTACTGTGTGAGAGTGTGAGGAGCAGTGTGACAGTGTGAGTGTGAGTGTGAGT 512
Db 361 CTGGGCTACTGTGTGAGAGTGTGAGGAGCAGTGTGACAGTGTGAGTGTGAGTGTGAGT 420
QY 513 CTTGAGGACTGTGTGACATCAACCTTCTAACTGTGTGAGTGTGAGTGTGAGTGTGAGT 572
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QY 573 GGGAGGAGAGATCGGTGTGTGCTCTACGAGCAGCAACTTCACTTCAAGTGTACT 632
Db 481 GGGAGGAGAGATCGGTGTGTGCTCTACGAGCAGCAACTTCACTTCAAGTGTACT 540
QY 633 CATCTCAGAGAGATCTCTGGGACCTGTGTGCTGAGCAGAGTGTGAGTGTGAGTGTGAGT 692
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QY 693 GGGGCGCTGAGGAGACATGGGCTATAGATATTTTACTTACCAAGAGTGTGAGTGTGAGT 752
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Db 721 ATAAAGAGCTGTACAGAGTGTGTCTTCAAGAGTGTGTCTTACGCTGTA 780
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QY 933 CGCTGCCGGGGGCTGGGCTGTGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 992
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QY 1233 AAACAGTGTGTGAGCAGCAGGATGTGATGTGAGCAGCAGCAGCAGCAGCAGCAGCAGT 1292
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Db	1740	TTCGCGAAGGGGTATGSGCGGCGTGGTGGGCACTGGGGGCGCAAGTGGGA - GGAAG	1799
QY	1891	GGGTGGAGGCGTG - CCCCATTGAGATTTCTCGCTGTAGTCTTTCCAGGGGCCAATTTTG	1949
Db	1800	GGTTGGAGGCGTGCCCCCATTTGAGATCTTCCTGTGTAGTCTTTCCAGGGGCCAATTTTG	1859
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Db	1860	ATGAGCATGTGAGCTGTCTACTTCTTCAGCTGCTGTGATGACTTGAATGAAAAAGAGAGACA	1919
QY	2010	TGCAAAAGGAGACAGCAGAGTGGCACCTGACAGGGCTG - CACTGGGGGCACCTGGTGT	2068
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Db	2215	CTGTGCATTTGGGTGGGGGCTCCGTGGGAGGAGACATCAGCCTTCTCTCATCTCTCCCTGA	2274
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Db	2392	AAATTCAGAGATGCTCAGTTTAAGTATCACTGTTTCCATGTTATGTTTCTACACATTTGAT	2450

RESULT 10
US-09-895-814-894
; Sequence 894, Application US/09895814
; Publication No. US20020193296A1

```

GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C26
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSeq for Version 3.0
SEQ ID NO 894
LENGTH: 2479
TYPE: DNA
ORGANISM: Homo sapiens
OS-09-895-814-894

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RESULT 11
US-09-759-143-894
; Sequence 894, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiaqun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.

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Db 1860 ATGAGCATGAGCTGTACACTCTCAGCTGTGATGATGATGAATGAAGGAAGAGACA 1919
Oy 2010 TGGAAAGGGAGACAGCCAGGTGACCTGTGACGGGCTG--CCTGTGGGGCCACTTGTAGT 2068
Db 1920 TGGAAAGGGAGACAGCCAGGTGACCTGTGACGGGCTGCCCTGTGGGGCCACTTGTAGT 1979
Oy 2069 GTCCCAAGCTTACTCTCCCAAGGGGATTTGCTGATGGGTTCTTAGAGCTTACAGC 2128
Db 1980 GTCCCAAGCTT--CTTCAAGGGGATTTTCTGATGGGTTCTTAGAGCTTACAGC 2036
Oy 2129 CTGGAATGAGGCGCAGAAATTAAGGGACAGCCCTCATGGGAGTGGATGAC 2188
Db 2037 CTGGAATGAGGCGCAGAAATTAAGGGACAGCCCTCATGGGAGTGGATGAC 2095
Oy 2189 CTGTGAAGGGGACAGAAACATTTTGTCTTATGGGGTGAATATAGACAGTGGCCTT 2248
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Db 2392 AATTCAGGATGCTCAGTTTAAAGTACACTGTTTCAATGTATGTTTCTACACATTTGT 2450

RESULT 14
US-10-012-896-930
Sequence 930, Application US/10012896
Publication No. US20020183251A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugui
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Veddyck, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Foy, Teresa
APPLICANT: Fanger, Gary R.
APPLICANT: Mantabe, Yoshhiro
APPLICANT: Meagher, Madeline Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.42/C27
CURRENT FILING DATE: US/10/012.896
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 930
LENGTH: 1479
TYPE: DNA
ORGANISM: Homo sapiens
US-10-012-896-930
Query Match 42.5%, Score 1464.8; DB 9; Length 1479;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1477; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
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DB 1 ATGGCTTGAAGTCAAGGACACCAAGTATGAGCTTACTATGAAACCATGATAC 60
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OY 329 TCCACCCCGTGTGTGACGAGCCCAATCCCATCCGGAGACGTGTGACCTTCAAG 388
DB 181 TCCACCCCGTGTGTGACGAGCCCAATCCCATCCGGAGACGTGTGACCTTCAAG 240
OY 389 ACTAAGAAAGCACTGTGATCACTTGAACCTTGGAGACCTTCTGTGGAGAGCTCGCTG 448
DB 241 ACTAAGAAAGCACTGTGATCACTTGAACCTTGGAGACCTTCTGTGGAGAGCTCGCTG 300
OY 449 GCCGCTGCTACTGTGAAGTTCAATGGGACAAAGTCTCCAACTGTGGATAGAGTGC 508
DB 301 GCCGCTGCTACTGTGAAGTTCAATGGGACAAAGTCTCCAACTGTGGATAGAGTGC 360
OY 509 GACTCTTAGTACTGATCAACCCCTTAACTGTGTGATGGGTGTCAACACTGCCCC 568
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DB 361 GACTCTTAGTACTGATCAACCCCTTAACTGTGTGATGGGTGTCAACACTGCCCC 420
OY 569 GCGGGGAGAGAGAGATCGTGTGTGCGCTCTACAGACCAACTTCATCTTCAGGTG 628
DB 421 GCGGGGAGAGAGAGATCGTGTGTGTGCGCTCTACAGATCAACTTCATCTTCAGGTG 480
OY 629 TACTCATCTCAGAGAGAGTCTGTGACCCCTGTGTGCCAAGACGACTGTGAACAGATAC 688
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DB 541 GGGGGGGGCTGAGAGGACATGGGCTATAGATATATTTTACTGTAGCCAGAGATA 600
OY 749 GTGATGACAGCGGATCCACAGCTTTATGAACAGCAAGTCCGCGCAATGTGAT 808
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OY 869 TGTATAGCTCGGGGCTGAATGACATCAAGCCGACAGAGAGATGTGGCGGCGAG 928
DB 721 TGTATAGCTCGGGGCTGAATGACATCAAGCCGACAGAGAGATGTGGCGGCGAG 780
OY 929 AGCGGCTCCCGGGGCTGCGGCTGCGGAGTCAAGCTGACAGTCCAGAAAGTCCAGT 988
DB 781 AGCGGCTCCCGGGGCTGCGGCTGCGGAGTCAAGCTGACAGTCCAGAAAGTCCAGT 839
OY 989 GTGCGAGGCTTCATCAATCAACCCCGAGTGTGTGACAGCCGCGCACTCGTGAAAA 1048
DB 840 GTGCGAGGCTTCATCAATCAACCCCGAGTGTGTGACAGCCGCGCACTCGTGAAAA 899
OY 1049 ACCCTTAACAATCATGAGCATGAGCAGCATTCGCGGAGATTTTGAACATCTTTAT 1108
DB 900 ACCCTTAACAATCATGAGCATGAGCAGCATTCGCGGAGATTTTGAACATCTTTAT 959
OY 1109 GTTCTATGAGCGGATACCAAGTAAAGTATTTCTATCCAAATTTATGATCCAA 1168
DB 960 GTTCTATGAGCGGATACCAAGTAAAGTATTTCTATCCAAATTTATGATCCAA 1019
OY 1169 GACCAAGAAATGATGATGCGGTGATGAGCTGACAGAGCTTCAAGACCT 1228
DB 1020 GACCAAGAAATGATGATGCGGTGATGAGCTGACAGAGCTTCAAGACCT 1079
OY 1229 AGTGAACAGTGTGTGCGCCCAACCCAGGATGTGTGACGCCAAGACGCTCTGCTG 1288
DB 1080 AGTGAACAGTGTGTGCGCCCAACCCAGGATGTGTGACGCCAAGACGCTCTGCTG 1139
OY 1289 GATTTCCGGGTGGGGGCGCACCGAGAGAAAGGAAAGTCTGAAAGTGTGAAAGCTGTC 1348
DB 1140 GATTTCCGGGTGGGGGCGCACCGAGAGAAAGGAAAGTCTGAAAGTGTGAAAGCTGTC 1199
OY 1349 CAAGTGTCTTCAATGAGACACAGAGATGCAACAGCATATGTCTATGCAACCTGAT 1408
DB 1200 CAAGTGTCTTCAATGAGACACAGAGATGCAACAGCATATGTCTATGCAACCTGAT 1259
OY 1409 CACACACAGCATATGATGTGCGGCTTCTGACAGGAGAACTGATTTCTCCAGAGTGA 1468
DB 1260 CACACACAGCATATGATGTGCGGCTTCTGACAGGAGAACTGATTTCTCCAGAGTGA 1319
OY 1469 CAGTGTGAGGCTTGTGTGACATTCGAAAGAAATTTGTGTGCTGATAGGAGATACAG 1528
DB 1320 CAGTGTGAGGCTTGTGTGACATTCGAAAGAAATTTGTGTGCTGATAGGAGATACAG 1379
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RESULT 15
US-09-895-793-930
; Sequence 930, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 930
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-930

Query Match          42.5%; Score 1464.8; DB 9; Length 1479;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1477; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 149 ATGGCTTTGAACACAGGAGTACACACAGCATTTGACCTTACTATGAAAAACATGATAC 208
DB 1 ATGGCTTTGAACACAGGAGTACACACAGCATTTGACCTTACTATGAAAAACATGATAC 60
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DB 301 GCCGCTGGCTTACTGTGAAGTTCATAGGAGCAGCAAGTGTCTCAACTCTGTGGATAGAGTGC 360
QY 509 GACTCTCAGGTACGATCAACCCCTCTCACTGATGATGGCGTGTACACTGCCCC 568
DB 361 GACTCTCAGGTACGATCAACCCCTCTCACTGATGATGGCGTGTACACTGCCCC 420
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QY 569 GGGGGGAGGACGAGATCGGTGTGTTCGCTCTACGACCAACTTCATCTTCAAGTGC 628
DB 421 GGGGGGAGGACGAGATCGGTGTGTTCGCTCTACGACCAACTTCATCTTCAAGTGC 480
QY 629 TACTCATCTCAGAGAGTCTGTGACCTGTGTGCCAGAGACATGGAAGAACATAC 688
DB 481 TACTCATCTCAGAGAGTCTGTGACCTGTGTGCCAGAGACATGGAAGAACATAC 540
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Thu Jan 16 09:33:07 2003

us-09-807-201-8.rnpb

Page 24

Search completed: January 16, 2003, 08:32:07
Job time : 1021 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 15, 2003, 08:39:45 ; Search time 44814 Seconds

(without alignments)
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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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41: em_hggo_other: *

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	3136.8	91.1	3245	6 AX201156	AX201156 Sequence
3	3136.8	91.1	3245	6 AX267955	AX267955 Sequence
4	3127.2	90.8	3226	6 AF329454	AF329454 Homo sapi
5	2309.4	67.1	2479	6 AX201121	AX201121 Sequence
6	2309.4	67.1	2479	6 AX207965	AX207965 Sequence
7	2309.4	67.1	2479	6 AX267920	AX267920 Sequence
8	2309.4	67.1	2479	6 AX306771	AX306771 Sequence
9	2309.4	67.1	2479	6 AX395318	AX395318 Sequence
10	2309.4	67.1	2479	9 HSU75329	U75329 Human serin
11	1769.4	51.4	60904	9 AC005612	AC005612 Homo sapi
12	1767.8	51.3	43003	9 HS87D5	AL773571 Homo sapi
13	1767.8	51.3	313064	17 HSMX1B	AL442167 Homo sapi
14	1763	51.2	108927	9 AP001609	AP001609 Homo sapi
15	1763	51.2	132110	9 AP001610	AP001610 Homo sapi
16	1763	51.2	340000	9 HS21C085	AL161285 Homo sapi
17	1712.4	49.7	1740	9 AF270487	AF270487 Homo sapi
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28	951.6	27.6	1735	10 AF243500	AF243500 Mus muscu
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ALIGNMENTS

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DEFINITION Sequence 3 from Patent WO0065067.
ACCESSION AX041973
VERSION AX041973.1 GI:11340738
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Nelson P.S., Hood L. and Lin B.
TITLE Prostate-specific polynucleotides, polypeptides and their methods
of use

Pred. No. is the number of results predicted by chance to have a

JOURNAL Patent: WO 0065067-A 3 02-NOV-2000;

The University of Washington (US)

FEATURES Location/Qualifiers

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BASE COUNT 992 a 998 c 988 g 984 t 4 others

ORIGIN

Query Match 94.0%; Score 3236.6; DB 6; Length 3966;

Best Local Similarity 99.1%; Pred. No. 0; Mismatches 18; Indels 9; Gaps 7;

Matches 3324; Conservative 4; Mismatches 18; Indels 9; Gaps 7;

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DB 1 GTCAATTTGAACATTCAGATACATATCATCTGATGCTGTGTATAACAGCAAGATG 60

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QY 333 ACCCGGTGTCTGCACGCAAGCCCAATCCCATCCGGGACAGTGTGCACCTCAAAAGCTA 392

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 REFERENCE 1 (bases 1 to 3245)
 AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
 Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
 Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
 TITILE Compositions and methods for the therapy and diagnosis of prostate
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1/29/03

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Db	61	GAGGCGCGCAGGTCATATTAAATTCACAGATACCATATCTACTGATGCTGTGATTA	120
QY	142	CAGCAAGATGGCTTTGAACTCAGAGGTCACACACAGCTATTTGACCTTACTATGA	201
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QY	682	GAATACGCGGCGGGCGCTGCAGAGGACATATGGCTTAAGAAATTAATTTTACTAC	741
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VERSION AX201121.1 GI:15390895
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ORGANISM Homo sapiens
human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolt,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
TITLE Compositions and methods for the therapy and diagnosis of prostate
cancer
JOURNAL Patent: WO 0151633-A 751 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 578 a 650 c 677 g 574 t
ORIGIN
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Db	601	GCGCGCGCTTGAGGAGCATATGGGCTATPAGAAATATTTTACTGTGCGCAAGGAATAGNG	660
QY	753	ATGACAGCGGATCCAGCAGGTTTATGAAACTGAAACAAGTCCCGCATGTGCATATCT	812
Db	661	ATGACAGCGGATCCAGCAGGTTTATGAAACTGAAACAAGTCCCGCATGTGCATATCT	720
QY	813	ATTAAMAACTGTACCAAGTAGTACCGCTTCTTCAAAACAGTGGTTTCTTACGCTATA	872
Db	721	ATTAAMAACTGTACCAAGTAGTACCGCTTCTTCAAAACAGTGGTTTCTTACGCTATT	780
QY	873	TAGCCTGGCGGGTCAACTTAACTCAAGCCGCGACAGACAGATCTGGGCGCGCAGACG	932
Db	781	TAGCCTGGCGGGTCAACTTGAAGTCAAGCGCGCAGACAGATCTGGGCGGTGAGNAGG	840
QY	933	CGCTCCGCGGGGCTGTGCCCTGGGCGAGTTCAGCTTCACAGATCTCACGCTGTGC	992
Db	841	CGCTCCGCGGGGCTGTGCCCTGGGCGAGTTCAGCTTCACAGATCTCACGCTGTGC	899
QY	993	GGAGGCTCATCATCACCCCCGAGTGGATGTATACAGCGCCACCTGCGTGGAAAAACT	1052
Db	900	GGAGGCTCATCATCACCCCCGAGTGGATGTATACAGCGCCACCTGCGTGGAAAAACT	959
QY	1053	CTTAAACAATCCATGCGATTGGACGGCAATTTGGGGGATTTTGAACAATCTTTCATGTTC	1112
Db	960	CTTAAACAATCCATGCGATTGGACGGCAATTTGGGGGATTTTGAACAATCTTTCATGTTC	1019
QY	1113	TATGGAGCGCGATCCAAAGTAGAAAAAGATTTCTCATCCAAATTAGATCCCAAGCC	1172
Db	1020	TATGGAGCGCGATCCAAAGTAGAAAAAGATTTCTCATCCAAATTAGATCCCAAGCC	1079
QY	1173	AGAACAATGACATTTGGCGTATGAAGCTGCAGAGACCTCTGACTTCAACGACCTATGT	1232
Db	1080	AGAACAATGACATTTGGCGTATGAAGCTGCAGAGACCTCTGACTTCAACGACCTATGT	1139
QY	1233	AAACAGTGTGTCTGCGCCAAACCAAGCGATATGTCTCAGCCAGAAACAGCTGTCTGATTT	1292
Db	1140	AAACAGTGTGTCTGCGCCAAACCAAGCGATATGTCTCAGCCAGAAACAGCTGTCTGATTT	1199

QY	1293	TCGGGTTGGGGGGCCACCGGAGGAGAAAGGAGAACTCAGAAAGTCTGAAGCTGCCAAG	1352
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QY	1353	GTGCTTCATTTGAGACACAGAGATGCACACAGAGATATGTCTATGACAACTGTATCA	1412
Db	1260	GTGCTTCATTTGAGACACAGAGATGCACACAGAGATATGTCTATGACAACTGTATCA	1319
QY	1413	CCAGCCATGATCTGTGCGGGCTTCCTGACAGGGGAACGTGCATTTCTTGACAGGTACAGT	1472
Db	1320	CCAGCCATGATCTGTGCGGGCTTCCTGACAGGGGAACGTGCATTTCTTGACAGGTACAGT	1379
QY	1473	GGAGGGGCTCTGGTCACTTGGAAAGCAATATCTGTGGCTATATGGGATATCAAGCTGG	1532
Db	1380	GGAGGGGCTCTGGTCACTTGGAAAGCAATATCTGTGGCTATATGGGATATCAAGCTGG	1439
QY	1533	GGTTCTGGCTGTGGCAAGCTTACAGCCAGAGGTATCGGGAATGTATGGTATTCAG	1592
Db	1440	GGTTCTGGCTGTGGCAAGCTTACAGCCAGAGGTATCGGGAATGTATGGTATTCAG	1499
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QY	1653	TCGTTTATCAAGAAACATATGGGGCTGTTTGCTCCCGTGACATTAATCTTAGA	1712
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Db	1860	ATGAGCATGAGAGCTGTACCTCTCAGCTCTGGATGACTTGGATGAGTAAAGAGAGACGA	1919
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ORGANISM	Homo sapiens		
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AUTHORS	1 Macbeth,K.J. and Shyjan,A.W.		
TITLE	Expressionalanalysis of specific nucleic acids and polypeptides useful in the diagnosis and treatment of prostate cancer		
JOURNAL	Patent: WO 0018961-A 4 06-Apr-2000;		
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QY	213	CGGAATAACCCCTATCCGCGACAGCCACTGTGTGCCCACTGTCTACGAGGTGATCCGG	272
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QY	273	CTCAGTACTACCCGTCGCCCGCTGCCCAAGTACGCCCCGAGGGTCTGTGACGACAGGCTTCCA	332
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QY	333	ACCCGCTGCTGCGACGAGACCCCAATATCCCATCCGCGGACAGTGTGACACTTAAGACATCA	392
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OY	453	CTGGCCTACTCTGGAAGTTTATGAGGGGAGCAAGAGCTCCAAAGCTGGGATAGAGTCCAGCT	512
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OY	573	GGGAGAGCAGAGATCGGTGTGTTCGCCCTACGGACCAATTCATCTTCAGGTGTACT	632
Db	481	GGGAGAGCAGAGATCGGTGTGTTCGCCCTACGGACCAATTCATCTTCAGGTGTACT	540
OY	633	CATCTCAGAGGAAGTCTGTGGCACCCTGTGTGTCCAAACACACTGTGAACGAACTACGGCC	692
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OY	693	GGGGGGCCCTGCAAGGACATGGGCTATAGAAATAATTTTACTGTAGCCAAAGAAATAGGG	752
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OY	753	ATGACAGCGGATCCACCAGCTTTATGAACTGAACAACAAGTCCCGCAATGTGCATATCT	812
Db	661	ATGACAGCGGATCCACCAGCTTTATGAACTGAACAACAAGTCCCGCAATGTGCATATCT	720
OY	813	ATTAACAACTGTACACAGATGATCCGTCTTCCAAACGAGTGTTTCTTTAGCGTGTGA	872
Db	721	ATTAACAACTGTACACAGATGATCCGTCTTCCAAACGAGTGTTTCTTTAGCGTGTGA	780
OY	873	TAGCCTGGGGGTAACCTTGAACTCAAGCCGCCAGAGCAGAACTGGGGCCGGCGAGACG	932
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OY	933	CGCTCCGGGGGCTGGCCCTTGGGCAAGTTCAGCTTCACAGAACGTCCTCACCTGTGC	992
Db	841	CGCTCCGGGGGCTGGCCCTTGGGCAAGTTCAGCTTCACAGAACGTCCTCACCTGTGC	899
OY	993	GGAGGCTCCATCATCACCCCCAGATGGATCTGTACACGCCGCCACTGCGTGGAAAACTT	1052
Db	900	GGAGGCTCCATCATCACCCCCAGATGGATCTGTACACGCCGCCACTGCGTGGAAAACTT	959
OY	1053	CTTAACATCCATGGCAATTGGACGGCAATTTGGGGGATTTTGAACAATCTTCACTGTTC	1112
Db	960	CTTAACATCCATGGCAATTGGACGGCAATTTGGGGGATTTTGAACAATCTTCACTGTTC	1019
OY	1113	TATGAGACCCGGAATCCAAAGTAGAAAAAGTATTTTCATCCAAATATATGATCCCAAGAC	1172
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OY	1233	AAACCAAGTGTCTGGCCCAACCCAGGATGATGCTGTGACACGAAACAGTCTGTGCGATTT	1292
Db	1140	AAACCAAGTGTCTGGCCCAACCCAGGATGATGCTGTGACACGAAACAGTCTGTGCGATTT	1199
OY	1293	TCCGGGTGGGGGGCCACCGAGAGAAAAAGGAACCTCAAGAGTGTGAAACCTCCCAAG	1352
Db	1200	TCCGGGTGGGGGGCCACCGAGAGAAAAAGGAACCTCAAGAGTGTGAAACCTCCCAAG	1259
OY	1353	GTGCTTCTCATTTGACACAGAGATGCAACAGCAGATATGTCTATGACAAACCTGTATACA	1412
Db	1260	GTGCTTCTCATTTGACACAGAGATGCAACAGCAGATATGTCTATGACAAACCTGTATACA	1319
OY	1413	CCAGCCATGATCTGTGCCGGCTTCTGTGCAAGGGGAACGTGATTTCTTGCAGGGGTACAGT	1472
Db	1320	CCAGCCATGATCTGTGCCGGCTTCTGTGCAAGGGGAACGTGATTTCTTGCAGGGGTACAGT	1379

Oy	753	ATGACAGGGATCCACAGGCTTTATGAAACTGTAACACAAAGTSCGGCAATGCGATATCT	812
Db	661	ATGCACAGGGATCCACAGGCTTTATGAAACTGTAACACAAAGTSCGGCAATGCGATATCT	720
Oy	813	ATAAAAACTGTATCCACAGATGATGCCCTGTTCTTCACAAACAGATGGTTCTTTACGCTGA	872
Db	721	ATAAAAACTGTATCCACAGATGATGCCCTGTTCTTCACAAACAGATGGTTCTTTACGCTGT	780
Oy	873	TAGCCTCGGGGGTCCAACTTGAACTCAAGCCGCCAGAGCAGATTCGTGGGGGGCGAGCG	932
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Oy	933	CGCTCCCGGGGGGCTGGCCCTGGGGGAGTCCAGCTCCAGATAGTCCAGATGCTCAGCTGTGC	992
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Oy	993	GGAGGCTCCATCATCAACCCCGAGTGGATGCTGTACAGCCGCCACCTGGCTGGAAAAACT	1052
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Oy	1053	CTTTAACATCCATGGCATTTGGACGCAATTTGGCGGGATTGTTGAGACAATCTTTCAATGTTTC	1112
Db	960	CTTTAACATCCATGGCATTTGGACGCAATTTGGCGGGATTGTTGAGACAATCTTTCAATGTTTC	1019
Oy	1113	TATGAGACCGGGATATCCAAAGTAAAGAAAAGTATTTCTCATCCAAATATATGATCCAAAGCC	1172
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Oy	1173	AAGAACTATGACATTTGGCGTGGATGAAGCTGTACAGAAAGCCCTGACTTTTCAAGCAAGCTACTG	1232
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Qy	1950	ATGAGCATGGAGCTGTACCTCTCAGCTCTGTGATGACTTGGATGAAAAAGAGACACA	2009
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DB 841 CGCTCCCGGGGGCCGTGGCGGTGAGAGTCAAGCTGCAGCTCCAGAAAGTGCACGTGTC 899
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DEFINITION sequence.
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VERSION AC005612.1 GI:3540153
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SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 60904)
AUTHORS Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
Kadner,K., Miquel,T., Miller,C., Pitluck,S., Pollard,M.,
Rojeski,H., Subramanian,S. and Martin,C.H.
TITLE Sequencing of human chromosome 21
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 60904)
AUTHORS Rhee,D.O.
TITLE Large Scale Sequence Analysis and Annotation with the Sequence
JOURNAL Comparison Analysis (SCAN) System
REFERENCE 3 (bases 1 to 60904)
AUTHORS Kimmerly,W., Bondoc,M., Cheng,J., Connolly,K.S., Gunning,K.M.,
Kadner,K., Miquel,T., Miller,C., Pitluck,S., Pollard,M.,
Rojeski,H., Subramanian,S. and Martin,C.H.
TITLE Direct Submission

JOURNAL Submitted (04-SEP-1998) Human Genome Center, DOE Joint Genome
Institute, Lawrence Berkeley National Laboratory, MS 74-157,
Berkeley, CA 94720, U.S.A.
COMMENT Sequence submitted by:
DOE Joint Genome Institute.
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	Matches 1818; Conservative	0; Mismatches 6; Indels 5; Gaps 4		
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AL773571.1 GI:21538699
KEYWORDS  HTG.
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE 1
Ramser,J., Francis,F., Beck,A., Hennig,S., Klages,S., Borzpm,K.,
Langer,I., Steffens,C., Hildmann,T., Dagand,E., Yaspo,M.,
Reinhardt,R. and Lehrach,H.
Unpublished
2 (bases 1 to 43003)
MPMG.
JOURNAL   Direct Submission
REFERENCE Submitted (01-OCT-1998) MPMG, Abt. Lehrach, Max Planck Institut
AUTHORS fuer Molekulare Genetik, Imnestrasse 73, Berlin, 14195, Germany
TITLE      Clones received from Resource Centre of the Human Genome Project at
COMMENT     the Max-Planck-Institut für Molecular Genetics.
            This submission was part of AL442167 and AJ011929
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Cancer Institute, creator: Pieter de Jong, P.Ioannou"
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D	284194	CACGTTTCCATGTTATGTTCTACATATGCTACCTCAGTGGCTCCCTGGAAACTTAGCTT	2841353
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D	283774	TGAATGGAAAGTCTTGCAATCCCATTTGGCAGATCCGTGTGCAATGCTCTGTGAGA	2837151
OY	2995	GAGCAGCAATTCACAGGACCTTGGAAACAGTTGGCACTGTAAAGTGTCTTCCCCAAAGA	3054
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OY 3355 CCCTCAGTTCTGTCAGCTGTCTGTGAGAGTCCCTCAATGACTCTTATATAT 3414
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RESULT 14
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LOCUS AP001609 Homo sapiens genomic DNA, chromosome 21, clone:KB447A5, MX1-D21S171
DEFINITION Homo sapiens genomic DNA, chromosome 21, clone:KB447A5, MX1-D21S171
region, complete sequence.
ACCESSION AP001609
VERSION AP001609.1 GI:7670563
KEYWORDS HNG.
SOURCE Homo sapiens pre-pro-B cell cell_line: FLEB14-14 DNA, clone: lib: Keio
BAC library clone: KB447A5.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 108927)
AUTHORS Shimizu, N., Kudoh, J. and Shibuya, K.
TITLE Homo sapiens genomic DNA, chromosome 21, clone: KB447A5, MX1-D21S171
region
JOURNAL Published Only in Database (2000)
REFERENCE 2 (bases 1 to 108927)
AUTHORS Shimizu, N., Kudoh, J. and Shibuya, K.
JOURNAL Submitted (04-APR-2000) Nobuyoshi Shimizu, Keio University, School
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160-8582, Japan (E-mail: nshimizu@med.keio.ac.jp,
Tel: 81-3-3351-2370, Fax: 81-3-3351-2370)
FEATURES
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ORIGIN

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LOCUS			Linear PRI 03-JUN-2000
DEFINITION			Homo sapiens genomic DNA, chromosome 21, clone:ClR2553B8.
ACCESSION			AP001610
VERSION			AP001610.1
KEYWORDS			GI:7670564
SOURCE			Htg.
ORGANISM			Homo sapiens sperm DNA, cloneLib:ClR-HSP BAC library clone:ClR2553B8.
REFERENCE			Homo sapiens
AUTHORS			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE			1 (bases 1 to 132110)
JOURNAL			Shimizu,N., Kudoh,J. and Shibuya,K.
REFERENCE			Submitted (04-APR-2000) Nobuyoshi Shimizu, Keio University, School of Medicine, Molecular Biology, 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582, Japan (E-mail:nshimizu@med.keio.ac.jp, Tel:81-3-3351-2370, Fax:81-3-3351-2370)
AUTHORS			Location/Qualifiers
JOURNAL			

Query Match	Best Local Similarity	Matches 1814; Conservative	51.2%; 99.2%; 0;	Score 1763; Pred. No. 0;	DB 9; Length 132110;	Indels 5;	Gaps
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